

CC retinopathy, hypertension, kidney disorders, angiogenesis-related
CC disorders, skin fibrotic disorders, and cardiovascular disorders. The
CC protein is also useful in wound healing, bone and tissue repair
XX
SQ Sequence 172 AA;

Query Match 100.0%; Score 956; DB 3; Length 172;

Best Local Similarity 100.0%; Pred. No. 1.7e-85; Indels 0; Gaps 0;
Matches 172; Conservative 0; Mismatches 0;

QY 1 ALAAVRLEDTFGPDPTMIRANCLVQTTWMSACSKTCGMGISTRTVNDNASCRLKQSRIC 60
DB 1 ALAAVRLEDTFGPDPTMIRANCLVQTTWMSACSKTCGMGISTRTVNDNASCRLKQSRIC 60
QY 61 MVRPCEADLEENIKKGGKCIPTPKISKPIKELSGCTSMKTYRAKFCGCTDGRCTPHR 120
DB 61 MVRPCEADLEENIKKGGKCIPTPKISKPIKELSGCTSMKTYRAKFCGCTDGRCTPHR 120
QY 121 TTTLPVBFKCPDGEVWKNMFIKTCACHYNCPGNDIFESLYRKMVGMA 172
DB 121 TTTLPVBFKCPDGEVWKNMFIKTCACHYNCPGNDIFESLYRKMVGMA 172

RESULT 2

AAW12694
ID AAW12694 standard; protein; 347 AA.

AAW12694;

XX 25-MAR-2003 (revised)
DT 31-MAY-1997 (first entry)

XX Connective tissue growth factor.

XX Connective tissue growth factor; CTGF; bone; cartilage; vulnery;
KW wound healing; osteoporosis; osteoarthritis; osteochondrytis.

OS Mus sp.

XX WO9638168-A1.

XX 05-DEC-1996.

XX 31-MAY-1996; 96WO-US008210.

XX 02-JUN-1995; 95US-00459717.

XX 31-MAY-1996; 96WO-US008140.

XX (GROT/) GROTEMDORST G R.

XX Grotenndorst GR;

XX WPI; 1997-042658/04.

XX N-PSDB; AAT59618.

XX Connective Tissue Growth Factor composition - for inducing bone, tissue
PT and cartilage formation and wound healing.

XX Disclosure; Fig 1C1-3; 60pp; English.

CC Connective tissue growth factor (CTGF) (AAW12694) is a cysteine-rich
CC mitogenic protein which is selectively induced in fibroblasts after
CC activation with transforming growth factor beta (TGF-beta). Recombinant
CC CTGF can be produced in prokaryotic or eukaryotic host cells utilizing an
CC isolated CTGF gene (AAT59618). Compsns. comprising CTGF, pref. in
CC combination with TGF-beta, are used to induce bonding formation, e.g. to
CC treat osteoporosis, osteoarthritis and osteochondrytis, to induce tissue
CC and cartilage formation, and to induce wound healing. It can also be used
CC in culture systems e.g. to expand stem cells or chondrocytes prior to re-
CC implantation. CTGF is more stable to protease degradation than other
CC growth factors used as prior art wound healing agents. (Updated on 25-MAR
CC -2003 to correct PR field.)
XX

SQ Sequence 347 AA;

Query Match 100.0%; Score 956; DB 2; Length 347;
Best Local Similarity 100.0%; Pred. No. 3.9e-85; Indels 0; Gaps 0;
Matches 172; Conservative 0; Mismatches 0;

QY 1 ALAAVRLEDTFGPDPTMIRANCLVQTTWMSACSKTCGMGISTRTVNDNASCRLKQSRIC 60
DB 176 ALAAVRLEDTFGPDPTMIRANCLVQTTWMSACSKTCGMGISTRTVNDNASCRLKQSRIC 235
QY 61 MVRPCEADLEENIKKGGKCIPTPKISKPIKELSGCTSMKTYRAKFCGCTDGRCTPHR 120
DB 236 MVRPCEADLEENIKKGGKCIPTPKISKPIKELSGCTSMKTYRAKFCGCTDGRCTPHR 295
QY 121 TTTLPVBFKCPDGEVWKNMFIKTCACHYNCPGNDIFESLYRKMVGMA 172
DB 296 TTTLPVBFKCPDGEVWKNMFIKTCACHYNCPGNDIFESLYRKMVGMA 347

RESULT 3

ABB09204
ID ABB09204 standard; protein; 348 AA.

ABB09204;

XX 08-JUL-2002 (first entry)

XX Human ctgF CNN family protein sequence SEQ ID NO:14.

XX Human; small CCN-like growth factor; SCGF; vulnery; osteopathic;
KW gene therapy; muscle wasting disease; osteoporosis; wound healing;

XX tissue regeneration; angiogenesis.

XX Homo sapiens.

XX US2002049304-A1.

XX 25-APR-2002.

XX 14-MAY-2001; 2001US-00853625.

XX 06-JUN-1995; 95US-00468847.

XX 01-APR-1998; 98US-00053587.

XX (HAST/) HASTINGS G A.

XX (ADAM/) ADAMS M D.

XX Hastings GA, Adams MD;

XX WPI; 2002-382150/41.

XX Novel isolated polynucleotide sequence encoding a human small CCN-like
PT growth factor, useful for treating muscle wasting disease, and
PT osteoporosis.

XX Disclosure; Fig 2A-D; 33pp; English.

CC The present invention describes human small CCN-like growth factor
CC (SCGF). SCGF has vulnery and osteopathic activities, and can be used in
CC gene therapy. The SCGF polypeptides and polynucleotides can be used for
CC treating muscle wasting diseases, and osteoporosis, and to stimulate
CC wound healing and tissue regeneration, to promote angiogenesis and to
CC stimulate proliferation of vascular smooth muscle and endothelial cell
CC production. The present sequence represents a CNN family protein which is
CC given in comparison with the human SCGF in the exemplification of the
CC present invention
XX

SQ Sequence 348 AA;

Query Match 100.0%; Score 956; DB 5; Length 348;
Best Local Similarity 100.0%; Pred. No. 3.9e-85; Indels 0; Gaps 0;
Matches 172; Conservative 0; Mismatches 0;

QY 1 ALAAVRLSDTGPDPPTMIRANCLVOTTEWSACSKTCGMSISTRYVNDNASCRLKQSRLC 60
 DB 177 ALAAVRLSDTGPDPPTMIRANCLVOTTEWSACSKTCGMSISTRYVNDNASCRLKQSRLC 236
 QY 61 MVRPEADLEENIKKGGKCIPTPKISKPIKELSGCTSMKTYRAFCGCTDGRCTPHR 120
 DB 237 MVRPEADLEENIKKGGKCIPTPKISKPIKELSGCTSMKTYRAFCGCTDGRCTPHR 296
 QY 121 TTTTPEVFEKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYYRKMGDMA 172
 DB 297 TTTTPEVFEKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYYRKMGDMA 348

RESULT 4
 AAR79964
 ID AAR79964 standard; protein; 349 AA.

XX AAR79964;

DT 25-MAR-2003 (revised)
 DT 12-JUN-1996 (first entry)

DE Connective tissue growth factor.

KM Connective tissue growth factor; CTGF; wound healing; vulnery; cell proliferation; cancer; fibrosis; atherosclerosis; diagnosis therapy; mitogen.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Modified-site 28 /label= N-glycosylation_site

FT Modified-site 225 /label= N-glycosylation_site

FN US5408040-A.

PD 18-APR-1995.

PF 14-DEC-1993; 93US-00167628.

PR 30-AUG-1991; 91US-00752427.

PA (UYSF-) UNIV SOUTH FLORIDA.

PI Bradham DM, Grotendorst GR;

XX WPI, 1995-161147/21.

DR N-PSDB; AAT04226.

PT New connective tissue growth factor - used to develop prod. for wound healing and for diagnosis and therapy of cell proliferative disorders.

PS Claim 1; Col 19-20; 12pp; English.

XX Novel human connective tissue growth factor (CTGF) (AAR79964) is related to immunologically and biologically to platelet-derived growth factor (PDGF), but is the product of a distinct gene. CTGF is mitogenic and also a chemotactic agent for cells. It is produced by endothelial and CC fibroblastic cells, and probably acts as a growth factor in wound healing. Recombinant CTGF can be obd. by expression of cDNA clone DB60832 (AAT04226) in transformed host cells. It is used to accelerate wound healing, and to raise antibodies useful in detecting disorders CC associated with overgrowth of cells, such as cancer, fibrotic diseases CC and atherosclerosis. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 349 AA;

Query Match 100.0%; Score 956; DB 2; Length 349;
 Best Local Similarity 100.0%; Pred. No. 3, 9e-85;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLSDTGPDPPTMIRANCLVOTTEWSACSKTCGMSISTRYVNDNASCRLKQSRLC 60
 DB 178 ALAAVRLSDTGPDPPTMIRANCLVOTTEWSACSKTCGMSISTRYVNDNASCRLKQSRLC 237
 QY 61 MVRPEADLEENIKKGGKCIPTPKISKPIKELSGCTSMKTYRAFCGCTDGRCTPHR 120
 DB 238 MVRPEADLEENIKKGGKCIPTPKISKPIKELSGCTSMKTYRAFCGCTDGRCTPHR 297
 QY 121 TTTTPEVFEKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYYRKMGDMA 172
 DB 298 TTTTPEVFEKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYYRKMGDMA 349

RESULT 5
 AAM11302
 ID AAM11302 standard; protein; 349 AA.

XX AAM11302;

DT 25-MAR-2003 (revised)
 DT 18-MAR-1997 (first entry)

DE Connective tissue growth factor.

KM Connective tissue growth factor; CTGF; human; connective tissue cell; proliferative disease; platelet-derived growth factor; PDGF; development; tissue growth; repair; umbilical vein endothelial cell; HUVE cell; antibody; wound healing; cancer; fibrotic disease; atherosclerosis; inhibitor; protease degradation; growth factor; therapy.

OS Homo sapiens.

PN US5585270-A.

PD 17-DEC-1996.

PF 10-FEB-1995; 95US-00386680.

PR 30-AUG-1991; 91US-00752427.

PR 14-DEC-1993; 93US-00167628.

PA (UYSF-) UNIV SOUTH FLORIDA.

PI Grotendorst GR, Bradham DM;

XX WPI, 1997-051180/05.

DR N-PSDB; AAT51234.

PT New nucleic acid encoding connective tissue growth factor - useful for accelerating wound healing, also for diagnosis and treatment of proliferative disease.

PS Claim 9; Col 15-18; 11pp; English.

XX This sequence represents the human connective tissue growth factor (CTGF). CTGF is related immunologically and biologically to platelet-derived growth factor (PDGF), but is encoded by an unrelated gene. CTGF is thought to play a significant role in the normal development, growth, CC and repair of human tissue, similarly to PDGF. The cDNA encoding this CC sequence was isolated by screening a cDNA library from human umbilical CC vein endothelial (HUVE) cells with anti-PDGF antibodies. CTGF can be used CC to accelerate wound healing. Also, elevated levels of CTGF may be CC diagnostic of proliferative diseases involving outgrowth of connective CC tissue cells, such as cancer, fibrotic disease and atherosclerosis. All CC of these diseases can be treated with reagents reactive with CTGF, such CC as antibodies (which can also serve as assay reagents). Antisense nucleic CC acids, and ribozymes could also be used to inhibit CTGF production. The CC advantage with using CTGF is that it is more stable, and less susceptible CC to protease degradation than PDGF, and other growth factors involved in CC wound healing. This is believed to be due to the high Cys content.
 (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 349 AA;

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Query Match      100.0%; Score 956; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 3.9e-85;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMSITRYTNDNASCRLEKOSRLC 60
DB 178 ALAAVRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMSITRYTNDNASCRLEKOSRLC 237
QY 61 MVRPEADLEENIKKGGKCI RTPKISKPIKFEISGCTSMKTYRAKFCGVCIDGRCTPHR 120
DB 238 MVRPEADLEENIKKGGKCI RTPKISKPIKFEISGCTSMKTYRAKFCGVCIDGRCTPHR 297
QY 121 TTTLPVFEKCPDGEVMMKNNMFIKTCACHYNCPEGNDIFESLYYRKMYGDMA 172
DB 298 TTTLPVFEKCPDGEVMMKNNMFIKTCACHYNCPEGNDIFESLYYRKMYGDMA 349

RESULT 6
AAW09089
ID AAW09089 standard; protein; 349 AA.
AC AAW09089;
XX
XX 25-MAR-2003 (revised)
DT 26-APR-1997 (first entry)
XX
DE Human connective tissue growth factor.
XX
XX Connective tissue growth factor; CTGF; mitogen; cell proliferation;
KW wound healing; cancer; tumour; fibrosis; glaucoma; atherosclerosis;
KW scleroderma; arthritis; cirrhosis; scar; diagnosis; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 28
FT /label= Glycosylation
FT /note= "potential N-glycosylation site"
FT Modified-site 225
FT /label= Glycosylation
FT /note= "potential N-glycosylation site"
XX
XX W06938172-A1.
XX
XX 05-DEC-1996.
PD
XX 31-MAY-1996; 96WO-US008140.
PF
XX 02-JUN-1995; 95US-00459717.
PR 31-MAY-1996; 96WO-US008140.
PR
XX (UYSF-) UNIV SOUTH FLORIDA.
PA
XX Grotenдорст GR, Bradham DM;
PI
XX WPI, 1997-042659/04.
DR N-PSDB; AAT45360, AAT58534.
DR
XX
XX Connective tissue growth factor coding sequence and protein - used in the
PT treatment of proliferative disorders and to accelerate wound healing.
PT
XX
XX Claim 19; Page 50-52; 76pp; English.
XX
XX Novel human connective tissue growth factor (CTGF) (AAW09089) is a PDGF-
CC immunorelated protein that may play a significant role in the normal
CC development, growth and repair of human tissue and probably functions as
CC a growth factor in wound healing. CTGF may be involved in diseases in
CC which there is an overgrowth of connective tissue cells, such as cancer,
CC tumour formation and growth, fibrotic diseases (e.g. pulmonary fibrosis,
CC kidney fibrosis, glaucoma) and atherosclerosis. Recombinant CTGF can be
CC produced in transformed host cells utilising a cDNA clone isolated from a
CC HUVEC library. It can be used to accelerate wound healing. CTGF
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CC inhibitors can be used to treat atherosclerosis and fibrotic diseases
CC such as scleroderma, arthritis, liver cirrhosis, and scarring. (Updated
CC on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 349 AA;
SQ
Query Match      100.0%; Score 956; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 3.9e-85;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMSITRYTNDNASCRLEKOSRLC 60
DB 178 ALAAVRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMSITRYTNDNASCRLEKOSRLC 237
QY 61 MVRPEADLEENIKKGGKCI RTPKISKPIKFEISGCTSMKTYRAKFCGVCIDGRCTPHR 120
DB 238 MVRPEADLEENIKKGGKCI RTPKISKPIKFEISGCTSMKTYRAKFCGVCIDGRCTPHR 297
QY 121 TTTLPVFEKCPDGEVMMKNNMFIKTCACHYNCPEGNDIFESLYYRKMYGDMA 172
DB 298 TTTLPVFEKCPDGEVMMKNNMFIKTCACHYNCPEGNDIFESLYYRKMYGDMA 349

RESULT 7
AAW62084
ID AAW62084 standard; protein; 349 AA.
AC AAW62084;
XX
XX 15-SEP-1998 (first entry)
DT
XX
DE Human connective tissue growth factor.
XX
XX Human; connective tissue growth factor; CTGF; PDGF; diagnosis; cancer;
KW platelet derived growth factor; ameliorating cell proliferative disorder;
KW atherosclerosis; fibrotic disease.
XX
XX Homo sapiens.
XX
XX US5783187-A.
XX
XX 21-JUN-1998.
PD
XX 11-SEP-1996; 96US-00712302.
PF
XX 30-AUG-1991; 91US-00752427.
PR 14-DEC-1993; 93US-00167628.
PR
XX (UYSF-) UNIV SOUTH FLORIDA.
PA
XX Bradham DM, Grotenдорст GR;
PI
XX WPI, 1998-426958/36.
DR N-PSDB; AAV38085.
DR
XX
XX Ameliorating cell proliferative disorder associated with connective
PT tissue growth factor - comprises the administration of an antibody which
PT binds to connective tissue growth factor and not to platelet-derived
PT growth factor.
PT
XX
XX Example 6; Col 17-20; 11pp; English.
XX
XX A method has been developed for ameliorating a cell proliferative
CC disorder associated with connective tissue growth factor (CTGF). The
CC method comprises the administration of an antibody or its fragment that
CC binds to CTGF and not to platelet-derived growth factor (PDGF), to the
CC site of the disorder. CTGF is related immunologically and biologically to
CC PDGF. The present sequence represents CTGF. The method is used to treat
CC conditions involving the overgrowth of connective tissue cells such as
CC cancer, atherosclerosis and other fibrotic diseases
XX
XX Sequence 349 AA;
```

Query Match 100.0%; Score 956; DB 2; Length 349;
 Best Local Similarity 100.0%; Pred. No. 3.9e-85;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLBETFGPDPMTIRANCLVQTTWMSACSKTCGMGISTRTVNDNASCRLEKQSRIC 60
 |||||
 DB 178 ALAAVRLBETFGPDPMTIRANCLVQTTWMSACSKTCGMGISTRTVNDNASCRLEKQSRIC 237
 |||||

QY 61 WVRPEADLEENIKKKKCIKRTPKISKPIKPELSGCTSMKTYRAKFCGCTDGRCTPHR 120
 |||||
 DB 238 WVRPEADLEENIKKKKCIKRTPKISKPIKPELSGCTSMKTYRAKFCGCTDGRCTPHR 297
 |||||

QY 121 TTTLPVEFKCPDGEVWKKMMFIKTCACHYNGPNDIFESLYYRKMVGDMA 172
 |||||
 DB 298 TTTLPVEFKCPDGEVWKKMMFIKTCACHYNGPNDIFESLYYRKMVGDMA 349
 |||||

RESULT 8
 AAWB1425
 ID AAWB1425 standard; protein; 349 AA.
 XX
 AC AAWB1425;
 XX
 DT 25-JAN-1999 (first entry)
 XX
 DE Connective tissue growth factor (CTGF).
 XX
 KW CTGF; connective tissue growth factor; bone formation; tissue; arthritis;
 wound healing; cartilage formation; osteoporosis; osteoarthritis; burn;
 osteochondritis; skeletal disorder; hypertrophic scar; protease; PDGF;
 degradation; vascular hypertrophy; platelet derived growth factor.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT Protein /note="signal peptide"
 FT Protein 22..349
 FT Protein /note="mature protein"

US5837258-A.
 17-NOV-1998.
 31-MAY-1996; 96US-00656393.
 30-AUG-1991; 91US-00752427.
 14-DEC-1993; 93US-00167628.
 10-FEB-1995; 95US-00386680.
 02-JUN-1995; 95US-00459717.
 (UYSF-) UNIV SOUTH FLORIDA.
 (UYMI-) UNIV MIAMI.
 Groendorst GR;
 MPI; 1999-023382/02.
 N-PSDB; AAV65380.

Use of connective tissue growth factor - for inducing bone, tissue or cartilage formation in a patient or for inducing wound healing.

Disclosure; Fig 1C; 30pp; English.

This represents the amino acid sequence of connective tissue growth factor (CTGF). This can be used in the method of the invention for inducing bone or tissue formation that comprises administration to a patient, a composition comprising CTGF and a carrier. CTGF can also be used in a method for inducing wound healing. The methods can be used for inducing bone, tissue or cartilage formation in disorders such as osteoporosis, osteoarthritis or osteochondritis, arthritis, skeletal disorders, hypertrophic scars, burns, vascular hypertrophy, or in wound healing. The CTGF and functional fragments are more stable and less

CC susceptible to protease degradation than platelet derived growth factor
 CC (PDGF) and other growth factors known to be involved in wound healing
 XX
 SQ Sequence 349 AA;

Query Match 100.0%; Score 956; DB 2; Length 349;
 Best Local Similarity 100.0%; Pred. No. 3.9e-85;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLBETFGPDPMTIRANCLVQTTWMSACSKTCGMGISTRTVNDNASCRLEKQSRIC 60
 |||||
 DB 178 ALAAVRLBETFGPDPMTIRANCLVQTTWMSACSKTCGMGISTRTVNDNASCRLEKQSRIC 237
 |||||

QY 61 WVRPEADLEENIKKKKCIKRTPKISKPIKPELSGCTSMKTYRAKFCGCTDGRCTPHR 120
 |||||
 DB 238 WVRPEADLEENIKKKKCIKRTPKISKPIKPELSGCTSMKTYRAKFCGCTDGRCTPHR 297
 |||||

QY 121 TTTLPVEFKCPDGEVWKKMMFIKTCACHYNGPNDIFESLYYRKMVGDMA 172
 |||||
 DB 298 TTTLPVEFKCPDGEVWKKMMFIKTCACHYNGPNDIFESLYYRKMVGDMA 349
 |||||

RESULT 9
 AAY18361
 ID AAY18361 standard; protein; 349 AA.
 XX
 AC AAY18361;
 XX
 DT 20-AUG-1999 (first entry)
 XX
 DE Human connective tissue growth factor.
 XX
 KW CTGF; connective tissue growth factor; human; fibrotic disease;
 cell proliferative disorder; atherosclerosis; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN US5916756-A.
 XX
 PD 29-JUN-1999.
 XX
 PF 20-JUN-1997; 97US-00880031.
 XX
 PR 14-DEC-1993; 93US-00167628.
 PR 10-FEB-1995; 95US-00386680.
 PR 11-SEP-1996; 96US-00712302.
 XX
 PA (UYSF-) UNIV SOUTH FLORIDA.
 XX
 PI Bradham DM, Groendorst GR;
 XX
 DR MPI; 1999-384720/32.
 DR N-PSDB; AAX61317.
 XX
 PT Detecting cell proliferative disorders such as fibrotic disease and
 PT atherosclerosis.
 XX
 PS Disclosure; Col 15-18; 11pp; English.
 XX
 CC This sequence is the human connective tissue growth factor (CTGF). The
 CC invention relates to a method of detecting a cell proliferative disorder
 CC comprising comparing the level of CTGF in a sample against a control,
 CC where an increase is indicative of a cell proliferative disorder
 CC (fibrotic disease or atherosclerosis). The method is used to detect cell
 CC proliferative disorders such as fibrotic disease and atherosclerosis
 XX
 SQ Sequence 349 AA;

Query Match 100.0%; Score 956; DB 2; Length 349;
 Best Local Similarity 100.0%; Pred. No. 3.9e-85;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLBETFGPDPMTIRANCLVQTTWMSACSKTCGMGISTRTVNDNASCRLEKQSRIC 60

DB 178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSTCGMGISTRTVTDNASCRLKQSRRLC 237
QY 61 MVRPCEADLEENIKKGGKCIPTPKISKPIKPELSGCTSMKTYRAKFCGVCCTDGRCCCTPHR 120
DB 238 MVRPCEADLEENIKKGGKCIPTPKISKPIKPELSGCTSMKTYRAKFCGVCCTDGRCCCTPHR 297
QY 121 TTTLPVEFKCPDGEVMMKMMFIKTGACCHYNCPGDNDIFESLYYRKMYGDMA 172
DB 298 TTTLPVEFKCPDGEVMMKMMFIKTGACCHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 10
AA92939
ID AA92939 standard; protein; 349 AA.
AC AAY92939;
XX 08-NOV-2000 (first entry)
DT
XX Human connective tissue growth factor protein.
DE
XX Dermatalogical; antiarthritic; antiarteriosclerotic; antidiabetic;
KM nephrotropic; ophthalmological; hypotensive; cardiac; tranquilizer;
KM vulnereary; antiinflammatory; human; connective tissue growth factor;
KM CTGF; extracellular matrix synthesis; collagen synthesis; antibody;
KM myofibroblast differentiation; antisense; fibroproliferative disease;
KM fibrosis; trauma; cancer; inflammation; diabetes; keloid.
XX
XX Homo sapiens.
OS
XX MO200035936-A1.
PN
XX 22-JUN-2000.
PD
XX 14-DEC-1999; 99WO-US029652.
PF
XX 14-DEC-1998; 98US-0112240P.
PR 14-DEC-1998; 98US-0112241P.
XX
XX (UTMI-) UNIV MIAMI.
PA
PI Groendorst GR;
XX
XX WPI; 2000-431565/37.
DR N-PSDB; AAA11278.
XX
XX Fragment of connective tissue growth factor, useful for treating
PT fibroproliferative diseases or disorders, including kidney fibrosis,
PT scleroderma, arthritis, hypertropic scarring, atherosclerosis, diabetic
PT nephropathy and retinopathy.
XX
XX Claim 2, 3; Fig 3A-B; 74pp; English.
PS
XX This sequence represents a human connective tissue growth factor (CTGF)
CC polypeptide having the ability to induce extracellular matrix synthesis,
CC collagen synthesis and/or myofibroblast differentiation. The invention
CC relates to fragments of CTGF, especially those encoded by exons 2 and/or
CC 3, which contain the inductive activity. The protein and/or fragments can
CC be used to raise antibodies and the coding sequence can be used to
CC generate antisense oligonucleotides. The antibody or antisense sequence
CC against the CTGF sequence can be used in a method to treat a CTGF-
CC associated disease or disorder such as a fibroproliferative disease or
CC disorder, especially selected from kidney fibrosis, scleroderma,
CC pulmonary fibrosis, liver fibrosis, arthritis, hypertropic scarring,
CC atherosclerosis, diabetic nephropathy and retinopathy, hypertension,
CC kidney disorders, angiogenesis-related disorders, skin fibrotic
CC disorders, and cardiovascular disorders. The disease or disorder can also
CC be selected from acute or repetitive traumas (including surgery or
CC radiation therapy, and fibrosis of organs), diseases caused by vascular
CC endothelial cell proliferation or migration (including cancers),
CC inflammatory bowel disease, Crohn's disease, joint inflammation,
CC interstitial disease, dermatological diseases, diabetes, and keloids

XX
SQ Sequence 349 AA;
Query Match 100.0%; Score 956; DB 3; Length 349;
Best Local Similarity 100.0%; Pred. No. 3.9e-85;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSTCGMGISTRTVTDNASCRLKQSRRLC 60
DB 178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSTCGMGISTRTVTDNASCRLKQSRRLC 237
QY 61 MVRPCEADLEENIKKGGKCIPTPKISKPIKPELSGCTSMKTYRAKFCGVCCTDGRCCCTPHR 120
DB 238 MVRPCEADLEENIKKGGKCIPTPKISKPIKPELSGCTSMKTYRAKFCGVCCTDGRCCCTPHR 297
QY 121 TTTLPVEFKCPDGEVMMKMMFIKTGACCHYNCPGDNDIFESLYYRKMYGDMA 172
DB 298 TTTLPVEFKCPDGEVMMKMMFIKTGACCHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 11
AA92940
ID AA92940 standard; protein; 349 AA.
AC AAY92940;
XX 08-NOV-2000 (first entry)
DT
XX Human connective tissue growth factor protein.
DE
XX Human; connective tissue growth factor; CTGF; mitogen; antibody; liver;
KM fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis;
KM hypertropic scarring; atherosclerosis; diabetic nephropathy; retinopathy;
KM hypertension; cardiovascular disorder; wound healing; bone repair.
XX
XX Homo sapiens.
OS
XX MO200035939-A2.
PN
XX 22-JUN-2000.
PD
XX 14-DEC-1999; 99WO-US029654.
PF
XX 14-DEC-1998; 98US-0112240P.
PR 14-DEC-1998; 98US-0112241P.
XX
XX (UTMI-) UNIV MIAMI.
PA (FIBR-) FIBROGEN INC.
PI Groendorst GR, Neff TB;
XX
XX WPI; 2000-431568/37.
DR N-PSDB; AAA11280.
XX
XX New fragment of connective tissue growth factor (CTGF) polypeptide having
PT mitogenic activity, useful in wound healing, bone and tissue repair.
XX
XX Claim 2, 3; Fig 2A-B; 71pp; English.
PS
XX This sequence represents a human connective tissue growth factor (CTGF)
CC polypeptide which has mitogenic activity. The protein can be used to
CC raise antibodies which specifically bind to CTGF and are used to treat a
CC CTGF-associated disease or disorder, e.g. a fibroproliferative
CC disease/disorder such as kidney fibrosis, scleroderma, pulmonary
CC fibrosis, liver fibrosis, arthritis, hypertropic scarring,
CC atherosclerosis, diabetic nephropathy and retinopathy, hypertension,
CC kidney disorders, angiogenesis-related disorders, skin fibrotic
CC disorders, and cardiovascular disorders. The protein is also useful in
CC wound healing, bone and tissue repair
XX
SQ Sequence 349 AA;
Query Match 100.0%; Score 956; DB 3; Length 349;

Best Local Similarity 100.0%; Pred. No. 3.9e-85;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLDTGPDPTMIRANCLVOTTEWSASCKTGMSISTRYTNDNASCRLEKQSRLC 60
DB 178 ALAAVRLDTGPDPTMIRANCLVOTTEWSASCKTGMSISTRYTNDNASCRLEKQSRLC 237
QY 61 MVRPCEADLEENIKKGGKCIKRTPKISKPIKEFLSGCTSMKTYRAKFCGCTDGRCTPPH 120
DB 238 MVRPCEADLEENIKKGGKCIKRTPKISKPIKEFLSGCTSMKTYRAKFCGCTDGRCTPPH 297
QY 121 TTTTLPVEFKCPDGEVWKKMMFMFKTCACHYNCPSGNDIFESLYYRKMGDMA 172
DB 238 TTTTLPVEFKCPDGEVWKKMMFMFKTCACHYNCPSGNDIFESLYYRKMGDMA 349

RESULT 12

AAV44755
ID AAV44755 standard; protein; 349 AA.

XX AAV44755;
AC

XX 04-MAY-2000 (first entry)
DT

XX Human connective tissue growth factor.
DE

XX Connective tissue growth factor; CN growth regulator; angiogenesis;
KW antiangiogenic; basic fibroblast growth factor; bFGF; neovascular;
KW endothelial cell proliferation; retinal; haemangioma; leukaemia;
KW metastasis; psoriasis; tumour; glaucoma; diabetic retinopathy; arthritis;
KW endometriosis; insulin-like growth factor-binding domain; IGF;
KW von Willebrand factor type C repeat; Thrombospondin type 1 domain;
KW C-terminal cysteine knot profile; CTCK-2; human.
XX

OS Homo sapiens.
XX

XX WO200005356-A1.
PN

XX 03-FEB-2000.
PD

XX 11-JUN-1999; 99WO-US013338.
PF

XX 21-JUL-1998; 98US-00119804.
PR

XX (CHIL-) CHILDRENS MEDICAL CENT.
PA

XX Folkmann J, Lin J;
PI

XX WPI; 2000-182668/16.
DR

XX New anti-angiogenic protein containing an IGF binding, Willebrand factor
PT type C, thrombospondin type 1 and cysteine knot domains is useful for
PT inhibiting atopic angiogenesis e.g. in solid tumors.
XX

XX Claim 6; Page 26-27; 30pp; English.
PS

XX The present sequence is human connective tissue growth factor, which is a
CC member of CN growth regulator family. It has antiangiogenic activity and
CC is a potent inhibitor of basic fibroblast growth factor (bFGF)-stimulated
CC bovine endothelial cell proliferation. It contains insulin-like growth
CC factor (IGF)-binding domain, von Willebrand factor type C repeat, CTCK-
CC Thrombospondin type 1 domain and C-terminal cysteine knot profile. (CTCK)-
CC 2 domain. It can be used to treat conditions associated with abnormal
CC angiogenesis or neovascularisation like, retinal neovascularisation,
CC tumour growth, haemangioma, solid tumors, leukaemia, metastasis,
CC psoriasis, neovascular glaucoma, diabetic retinopathy, arthritis,
CC endometriosis and premature retinopathy
CC

XX Sequence 349 AA;
SQ

Query Match 100.0%; Score 956; DB 3; Length 349;
Best Local Similarity 100.0%; Pred. No. 3.9e-85;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLDTGPDPTMIRANCLVOTTEWSASCKTGMSISTRYTNDNASCRLEKQSRLC 60
DB 178 ALAAVRLDTGPDPTMIRANCLVOTTEWSASCKTGMSISTRYTNDNASCRLEKQSRLC 237

QY 61 MVRPCEADLEENIKKGGKCIKRTPKISKPIKEFLSGCTSMKTYRAKFCGCTDGRCTPPH 120
DB 238 MVRPCEADLEENIKKGGKCIKRTPKISKPIKEFLSGCTSMKTYRAKFCGCTDGRCTPPH 297
QY 121 TTTTLPVEFKCPDGEVWKKMMFMFKTCACHYNCPSGNDIFESLYYRKMGDMA 172
DB 238 TTTTLPVEFKCPDGEVWKKMMFMFKTCACHYNCPSGNDIFESLYYRKMGDMA 349

RESULT 13

AAB84598
ID AAB84598 standard; protein; 349 AA.

XX AAB84598;
AC

XX 05-SEP-2001 (first entry)
DT

XX Amino acid sequence of connective tissue derived growth factor.
DE

XX Growth factor; protein inhibitor; protease; damaged tissue;
KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
KW vascular endothelial growth factor; urokinase plasminogen activator;
KW dermal ulcer; wound.
XX

OS Homo sapiens.
XX

XX WO200149309-A2.
PN

XX 12-JUL-2001.
PD

XX 21-DEC-2000; 2000WO-1B001935.
PF

XX 29-DEC-1999; 99GB-00030768.
PR

XX (PF12) PFIZER LTD.
PA

XX (PF12) PFIZER INC.
PA

XX Davies MJ, Huggins JP, McIntosh FS, Occlleston NL;
PI

XX WPI; 2001-418351/44.
DR

XX N-PSDB; AAR28213.
DR

XX Composition for the treatment of damaged tissue i.e. chronic wounds and
PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
PT factor.
XX

XX Disclosure; Page 543; 572pp; English.
PS

XX The specification describes a pharmaceutical composition, comprising a
CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
CC inhibits the action of at least one specific adverse protein, i.e. a
CC protease, that is upregulated in a damaged tissue such as a wound
CC environment. Growth factors which are included in the composition of the
CC invention are platelet-derived growth factor (PDGF), fibroblast growth
CC factor (FGF), connective tissue derived growth factor (CTGF), factor-beta
CC keratinocyte-derived growth factor (KGF), transforming growth factor (TGF-beta),
CC granulocyte macrophage colony stimulating factor (GM-CSF),
CC (TGF-beta), granulocyte macrophage colony stimulating factor (VEGF),
CC epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
CC and chrysalin. Inhibitors which are included in the composition of the
CC invention include inhibitors of urokinase-type plasminogen activator
CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for
CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
CC The present sequence represents a human CTGF, and is used to produce the
CC composition of the invention

OY	61	MVRPCBADLEBNIKKGGKCI	RTPKISKPIKPEL	SGCTSMKTYRAK	CGVCTDGRCTPHR	120
Db	238	MVRPCBADLEBNIKKGGKCI	RTPKISKPIKPEL	SGCTSMKTYRAK	CGVCTDGRCTPHR	297
OY	121	TTTLPEVEFKCPDGEVMMKMM	FIKTCACHYNC	PGDNDIFESL	YXRMYGDMA	172
Db	298	TTTLPEVEFKCPDGEVMMKMM	FIKTCACHYNC	PGDNDIFESL	YXRMYGDMA	349

Search completed: January 9, 2006, 11:16:16
Job time : 136 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2006, 11:11:27 ; Search time 40 Seconds

(without alignments)
413.732 Million cell updates/sec

Title: US-09-461-646-4

Perfect score: 956
Sequence: 1 ALAAVRLBDTFFGDPPTMIRA.....PGDNDIFSLYRRKMGDMA 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	956	100.0	349	2 A40551	connective tissue
2	934	97.7	348	2 A40578	beta IG-M2 protein
3	546.5	57.2	351	2 S20078	NOV protein - chic
4	543.9	54.3	357	2 I38069	gene novh protein
5	487.5	51.0	379	2 A35669	gene CTR61 protein
6	479.5	50.2	375	2 A41428	CBF-10 protein pre
7	116	12.1	2165	2 T21371	hypothetical prote
8	107	11.2	1444	2 T18856	angiogenesis inhib
9	102.5	10.7	2098	2 T18397	protein CTRP - mal
10	101.5	10.6	807	2 A38152	F-spondin - rat
11	99.	10.4	712	2 A45638	immunodominant mic
12	99	10.4	803	2 A47423	F-spondin precursor
13	97	10.1	4753	1 A47437	LDL-receptor-relat
14	96.5	10.1	654	2 T29247	hypothetical prote
15	96.5	10.1	898	2 T14764	hypothetical prote
16	92	9.6	1205	2 T18517	procollagen N-endo
17	92	9.6	1274	2 T42017	hypothetical rich prot
18	91	9.5	1059	2 T22545	hypothetical prote
19	90.5	9.5	651	2 T19477	mucin SAC (clone L
20	90.5	9.5	1042	2 A57534	hypothetical prote
21	90.5	9.5	1372	2 T25933	hypothetical prote
22	90.5	9.5	4006	2 T09070	probable tenascin
23	89.5	9.4	388	2 A39786	circumsporozoite p
24	89.5	9.4	1178	1 A39804	thrombospondin pre
25	89	9.3	1558	2 C89114	protein C37C3.6a l
26	89	9.3	2167	2 T34395	hypothetical prote
27	88.5	9.2	104	2 S50911	metallothionein-2
28	88	9.2	1025	2 T42656	secreted leucine-r
29	88	9.2	2910	2 T42214	ocogelin - mouse

30	87.5	9.2	412	1 OZ2QAF	circumsporozoite p
31	87.5	9.2	424	2 A54533	circumsporozoite p
32	87.5	9.2	442	2 A54529	circumsporozoite p
33	87.5	9.2	957	2 T15976	hypothetical prote
34	87	9.1	152	2 I47109	high-sulfur wool m
35	87	9.1	732	2 S47073	finger protein HZF
36	87	9.1	837	2 A42112	mucin-like peptide
37	87	9.1	1170	2 TSHUP1	thrombospondin 1 p
38	86	9.0	388	2 JG6164	circumsporozoite p
39	86	9.0	951	2 T00260	hypothetical prote
40	86	9.0	1170	2 A40558	thrombospondin 1 p
41	85.5	8.9	724	2 A48569	antigen Bm100 - Bi
42	85	8.9	111	2 T34565	hypothetical prote
43	85	8.9	152	2 KRSHHC	keratin high-sulfu
44	85	8.9	152	2 I47112	high-sulfur wool m
45	85	8.9	182	2 I47105	high-sulfur wool m

ALIGNMENTS

RESULT 1
A40551
connective tissue growth factor - human
C/Species: Homo sapiens (man)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Dec-2004
C/Accession: A40551; S44205
R/Bradham, D.M.; Igarashi, A.; Potter, R.L.; Grotenhorst, G.R.
J. Cell Biol. 114, 1285-1294, 1991
A/Title: Connective tissue growth factor: a cysteine-rich mitogen secreted by human vas.
A/Reference number: A40551; MUID:91373462; PMID:1654338
A/Accession: A40551
A/Molecule type: mRNA
A/Residues: 1-349

A/Cross-references: UNIPROT:P29279; UNIPARC:UPI000003FD13; GB:M92934; GB:M36965; GB:S56.
R/Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Genetz, R.; Luescher, T.F.
submitted to the EMBL Data Library, April 1994
A/Description: Differential cloning and expression of human connective tissue growth fac
A/Reference number: S44205
A/Accession: S44205
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-349 <OEM>
A/Cross-references: UNIPARC:UPI000003FD13; EMBL:X78947; NID:G474933; PID:G474934
C/Superfamily: IGFBP-related protein, CNN type

Query Match 100.0%; Score 956; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 1e-76;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLBDTFFGDPPTMIRANCLVOTTEWSACGKTGGMGISTPVYTNDAASCRIEKOSRLC 60
|||||
DB 178 ALAAVRLBDTFFGDPPTMIRANCLVOTTEWSACGKTGGMGISTPVYTNDAASCRIEKOSRLC 237
|||||

QY 61 MWPRCEADLEBNIKKGGKICRTPKISKPIFELSGLCTSMKTYRAKCGVCTDGRCCTPHR 120
|||||
DB 238 MWPRCEADLEBNIKKGGKICRTPKISKPIFELSGLCTSMKTYRAKCGVCTDGRCCTPHR 297
|||||

QY 121 TTTLPVFEKCPDGEVKKMMFPIKTCACHYNCGDNDIFSLYRRKMGDMA 172
|||||
DB 298 TTTLPVFEKCPDGEVKKMMFPIKTCACHYNCGDNDIFSLYRRKMGDMA 349
|||||

RESULT 2
A40578
beta IG-M2 protein precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 31-Dec-2004
C/Accession: A40578; A53228
R/Brummer, A.; Chinn, J.; Neubauer, M.; Purchio, A.F.
DNA Cell Biol. 10, 293-300, 1991
A/Title: Identification of a gene family regulated by transforming growth factor-beta.
A/Reference number: A40578; MUID:91229699; PMID:2029337

A:Accession: A40578
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-348 <BRU>
A:Cross-references: UNIPROT:P29268; UNIPARC:UP10000028AE; GB:M80263; NID:g201945; PIDN:
R:Rybeck, R.P.; Macdonald-Bravo, H.; Mattei, M.G.; Bravo, R.
Cell Growth Differ. 2, 225-233, 1991
A:Title: Structure, mapping, and expression of fisp-12, a growth factor-inducible gene
A:Reference numbers: A53228; MUID:91363290; PMID:1888698
A:Accession: A53228
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-160, 'K', 162-348 <RYS>
A:Cross-references: UNIPARC:UP1000003PD12; GB:M70641; NID:g193313; PIDN:AAA37627.1; PID:
C:Genetics:
A:Gene: fisp-12
C:Superfamily: IGFBR-related protein, CNN type

Query Match 97.7%; Score 934; DB 2; Length 348;
Best Local Similarity 95.9%; Pred. No. 8.8e-75;
Matches 165; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ALAAVRLDTPGDPPTMIRANCLVOTTEWSACSKTCGMGISTRTVNDNASCRLKQSLIC 60
Db 177 ALAAVRLDTPGDPPTMIRANCLVOTTEWSACSKTCGMGISTRTVNDNTPCRLKQSLIC 236
Oy 61 MVRPEADLEENIKKGGKCIKRTPKISKIPKELSGCTSMKTYRAKFCGVCCTDGRCTPHR 120
Db 237 MVRPEADLEENIKKGGKCIKRTPKIAKPVKELSGCTSVKTYRAKFCGVCCTDGRCTPHR 296
Oy 121 TTTLPVEFKCPDGEVMMKMMFIKTCACHYNCPGNDIFESLYRYKMGDMA 172
Db 297 TTTLPVEFKCPDGEVMMKMMFIKTCACHYNCPGNDIFESLYRYKMGDMA 348

RESULT 3

S20078
NOV protein - chicken
C:Species: Gallus gallus (chicken)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
C:Accession: S20078
R:Joliet, V.; Martinerie, C.; Dambrine, G.; Plassiart, G.; Brisac, M.; Crochet, J.; Perh
Mol. Cell. Biol. 12, 10-21, 1992
A:Title: Proviral rearrangements and overexpression of a new cellular gene (nov) in myel
A:Reference numbers: S20078; MUID:92107157; PMID:1309586
A:Accession: S20078
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-351 <JOL>
A:Cross-references: UNIPROT:P28686; UNIPARC:UP100001303BC; EMBL:X59284; NID:g63702; PIDN:
C:Genetics:
A:Gene: NOV
C:Superfamily: IGFBR-related protein, CNN type

Query Match 57.2%; Score 546.5; DB 2; Length 351;
Best Local Similarity 59.7%; Pred. No. 1e-40; Indels 1; Gaps 1;
Matches 95; Conservative 23; Mismatches 40;

Oy 1 ALAAVRLDTPGDPPTMIRANCLVOTTEWSACSKTCGMGISTRTVNDNASCRLKQSLIC 60
Db 191 AMAAVRLDTPGDPPTMIRANCLVOTTEWSACSKTCGMGISTRTVNDNASCRLKQSLIC 240
Oy 61 MVRPEADLEENIKKGGKCIKRTPKISKIPKELSGCTSMKTYRAKFCGVCCTDGRCTPHR 120
Db 241 MVRPEADLEENIKKGGKCIKRTPKISKIPKELSGCTSMKTYRAKFCGVCCTDGRCTPHR 299
Oy 121 TTTLPVEFKCPDGEVMMKMMFIKTCACHYNCPGNDIF 159
Db 300 TTTLPVEFKCPDGEVMMKMMFIKTCACHYNCPGNDIF 338

RESULT 4

138069

gene novH protein - human
C:Species: Homo sapiens (man)
C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 31-Dec-2004
C:Accession: I38069
R:Martinerie, C.; Huff, V.; Joubert, I.; Badziach, M.; Saunders, G.; Strong, L.; Perbal,
Oncogene 9, 2729-2732, 1994
A:Title: Structural analysis of the human nov proto-oncogene and expression in Wilms tum
A:Reference numbers: I38069; MUID:94336229; PMID:7520150
A:Accession: I38069
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-357 <RES>
A:Cross-references: UNIPROT:P48745; UNIPARC:UP100001303BE; EMBL:X78351; NID:g587422; PID:
C:Genetics:
A:Gene: novH
A:Introns: 28/3; 104/1; 188/1; 259/3
C:Superfamily: IGFBR-related protein, CNN type
F:203-250/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 54.3%; Score 519; DB 2; Length 357;
Best Local Similarity 54.7%; Pred. No. 2.7e-38;
Matches 94; Conservative 25; Mismatches 51; Indels 2; Gaps 2;

Oy 2 LAAYRLDTPGDPPTMIRANCLVOTTEWSACSKTCGMGISTRTVNDNASCRLKQSLIC 61
Db 186 LAAYRLDTPGDPPTMIRANCLVOTTEWSACSKTCGMGISTRTVNDNASCRLKQSLIC 245
Oy 62 VVRPEADLEENIKKGGKCIKRTPKISKIPKELSGCTSMKTYRAKFCGVCCTDGRCTPHR 120
Db 246 VVRPEADLEENIKKGGKCIKRTPKISKIPKELSGCTSMKTYRAKFCGVCCTDGRCTPHR 305
Oy 121 TTTLPVEFKCPDGEVMMKMMFIKTCACHYNCPGNDIF-ESLYRYKMGDMA 171
Db 306 TTTLPVEFKCPDGEVMMKMMFIKTCACHYNCPGNDIF-ESLYRYKMGDMA 357

RESULT 5

A35669
gene CYR61 protein precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 31-Dec-2004
C:Accession: A35669; I48319; S16446
R:O'Brien, T.P.; Yang, G.P.; Sanders, L.; Lau, L.F.
Mol. Cell. Biol. 10, 3569-3577, 1990
A:Title: Expression of cyr61, a growth factor-inducible immediate-early gene.
A:Reference numbers: A35669; MUID:90287146; PMID:2355916
A:Accession: A35669
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-379 <OAB>
A:Cross-references: UNIPROT:P16406; UNIPARC:UP1000022DPF; GB:M32490; NID:g192909; PIDN:
A>Note: the authors translated the codon GAT for residue 337 as Gln
Nucleic Acids Res. 19, 3261-3267, 1991
A:Title: Promoter function and structure of the growth factor-inducible immediate early
A:Reference numbers: I48319; MUID:91288203; PMID:2062642
A:Accession: I48319
A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-379 <RES>
A:Cross-references: UNIPARC:UP1000022DPF; EMBL:X56790; NID:g50632; PIDN:CAA40109.1; PID
A>Note: the authors did not translate the codon for residue 108
A>Note: the authors translated the codon GAT for residue 337 as Gln
C:Genetics:
A:Gene: CYR61
A:Introns: 21/3; 93/1; 208/1; 279/3
C:Superfamily: IGFBR-related protein, CNN type
F:99-166/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 51.0%; Score 487.5; DB 2; Length 379;
Best Local Similarity 49.4%; Pred. No. 1.7e-35;
Matches 83; Conservative 32; Mismatches 44; Indels 9; Gaps 2;

11 FGPPPTMI-----RANCLVQTTWESWASCTTCGMSGISTRVTNNASCRLEKOSRLCMVR 63
 A:Cross-references: UNIPROT:P19336; UNIPARC:UPI0000127478; GB:J04496; MID:G211435; PIDN
 C:Superfamily: IGFBP-related protein, CNN type
 Query Match 50.2%; Score 479.5; DB 2; Length 375;
 Best Local Similarity 51.3%; Pred. No. 8.3e-35;
 Matches 81; Conservative 27; Mismatches 45; Indels 5; Gaps 2;
 Db 11 FGPPPTMI-----RANCLVQTTWESWASCTTCGMSGISTRVTNNASCRLEKOSRLCMVR 67
 210 FGSEQGSAPENPKIVQTTWSQCSKTCGTGISTRVTNDNDPCLIKETRIICVRPCGQ 269
 68 DLEENIKKKKKCIRTPTKISKPIKEFLSGCTSMKTYRAKFCGVCITDGRCTPHRTTLEVE 127
 270 PSYALKKKGKCTCTTKKSPSPVRFTYAGCSVKKYRPYCGSCVDGRCTPQGTFTVKIR 329
 QY 128 FKCPDGEVMMKKMMFIKTCACHYNGPGNDIFESLYYR 165
 330 FRCDGETFTYSVMVMIQSCRCNYNCPHANEAVP--FYR 365
 Db 330 FRCDGETFTYSVMVMIQSCRCNYNCPHANEAVP--FYR 365
 RESULT 7
 T21371
 hypochetrical protein F25H8.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T21371; T24896
 R:Gajadary, S.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: Z19413
 A:Accession: T21371
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Reads: 1-2165 «W11»
 A:Cross-references: UNIPROT:Q19791; UNIPARC:UPI000007CF95; EMBL:Z69360; PIDN:CAA93287.1
 R:Experimental source: clone F25H8
 submitted to the EMBL Data Library, February 1996
 A:Reference number: Z19949
 A:Accession: T24896
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Reads: 1-2165 «W12»
 A:Cross-references: UNIPARC:UPI000007CF95; EMBL:Z69361; PIDN:CAA93288.1; GSPDB:GN00022;
 A:Experimental source: clone T13H10
 C:Genetics:
 A:Gene: CESP:F25H8.3

[illegible]

Mol. Biochem. Parasitol. 74, 129-142, 1995
A:Title: Molecular cloning of a gene from Plasmodium falciparum that codes for a protein
A:Reference number: 218926; MUID:96360477; PMID:8719155
A:Accession: 118397
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2098 <TRO>
A:Cross-references: UNIPROT:Q25757; UNIPARC:UPI000008040C; EMBL:U34363; NID:g1098897; P4

Query Match 10.7%; Score 102.5; DB 2; Length 2098;
Best Local Similarity 23.8%; Pred. No. 0.55;
Matches 40; Conservative 21; Mismatches 52; Indels 55; Gaps 10;

Qy 28 EMSACSTCGGISTRTVNDNA-----SCRLEKOSRL--CMVRPCE---ADLEENIKK- 75
Db 1586 EWSSECSATCGGIRNR-NRDSLNDNDCKLPNSTEMACIQICEDDNNVDCIEDIGEW 1644
F:444-455/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:1557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

RESULT 10
A38152
F-spondin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A38152
R:Klar, A.; Baldaasare, M.; Jessell, T. M.
Cell 69, 95-110, 1992
A:Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secreted
A:Reference number: A38152; MUID:92208952; PMID:1555244
A:Accession: A38152
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-807 <KLA>
A:Cross-references: UNIPROT:P35446; UNIPARC:UPI000012AC71; GB:M88469; NID:g204176; PIDN:
A:Experimental source: embryo floor plate
A:Note: sequence extracted from NCBI backbone (NCBIN:90877; NCBI:P:90878)
C:Superfamily: F-spondin: thrombospondin type 1 repeat homology
F:444-455/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:1557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match 10.6%; Score 101.5; DB 2; Length 807;
Best Local Similarity 24.7%; Pred. No. 0.28;
Matches 42; Conservative 19; Mismatches 46; Indels 63; Gaps 10;

Qy 20 ANCIY-QTTMSAGSKTCGMGSTR-----VTNDNASCRLK-QSRLCMVRPCE----- 66
Db 557 SSCIVTEGEMWDDCATCGMKKRRHVRKSPADGSCCKETSQAEKCMPECTITICL 616
F:444-455/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:1557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Qy 67 -----ADLEENIKKGGKCTRTPIKSPKIFELSG 95
Db 617 LSPNEMSDCSVTGCKMRTQRMLKSLAELGDCNEDLEQAKCM-LPEC--PIDCEISE 673
F:444-455/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:1557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Qy 96 CTSMKTYRAKFCGCTDGRCTPH--RTTTLPEV-----FKCPDGEVMKK 138
Db 674 WSGMECN-KSCG-----KGHWIRTTIOMEPOFGAPCEPVTORRK 714
F:444-455/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:1557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

RESULT 11
A45638
Immunodominant microneme protein Eip100 - Eimeria tenella
C:Species: Eimeria tenella
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A45638
R:Tomey, F. M.; Parastol, L. E.; Kawazoe, U.; Dijkema, R.; Kok, J. J.
Mol. Biochem. Parasitol. 49, 277-288, 1991
A:Title: Sequence of the gene encoding an immunodominant microneme protein of Eimeria ter
A:Reference number: A45638; MUID:92131064; PMID:1775171
A:Accession: A45638
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-712 <TOM>
A:Cross-references: UNIPROT:Q43981; UNIPARC:UPI00000788B2; GB:AF032905; GB:M73495; NID:g4
A:Note: sequence extracted from NCBI backbone (NCBIN:77752; NCBI:P:77756)
F:48-218/Domain: von Willebrand factor type A repeat homology <VWA1>
F:238-296/Domain: thrombospondin type 1 repeat homology <THR1>
F:309-371/Domain: thrombospondin type 1 repeat homology <THR2>
F:372-432/Domain: thrombospondin type 1 repeat homology <THR3>
F:433-493/Domain: thrombospondin type 1 repeat homology <THR4>
F:494-556/Domain: thrombospondin type 1 repeat homology <THR5>
F:560-610/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match 10.4%; Score 99; DB 2; Length 712;
Best Local Similarity 24.0%; Pred. No. 0.41;
Matches 47; Conservative 19; Mismatches 66; Indels 64; Gaps 11;

Qy 14 DPTMIRANCLVQTTMSAGSKTCGMGISTRTVN---DNA-----SCRLEK-----OSRL 59
Db 429 NPCPIDATC-GEWTEYACSGRTCGGTQERKRBEWMLDNAHGRTC-MEYPPDGPISVRE 486
F:444-455/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:1557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Qy 60 CMVRPCEAD-----LEENIKKGGK-----IRTPKISK 87
Db 487 CNTQPCVDEVDGDMEDMGCCSEGGCKTRNRGSPKQEMRGKTVVAQNMALPEGEK 546
F:444-455/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:1557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Qy 88 PIKELSGCTSMKTYRAKFCGVC-----TDGRCTPHRTTTLPEVFKCPDGEVMKKM 140
Db 547 IEVQBERGCHVP-----GGPCTLPSEWTEGSCSGHRTREBAVAFDYTD-RMCGDTR 599
F:444-455/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:1557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Qy 141 MFITCA--CHYCPG 154
Db 600 HEVQSCREYCSQNNAG 615
F:444-455/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:1557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

RESULT 12
A47723
F-spondin precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A47723
R:Ruiz i Altaba, A.; Cox, C.; Jessell, T. M.; Klar, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A:Title: Ectopic neural expression of a floor plate marker in frog embryos injected with
A:Reference number: A47723; MUID:93376785; PMID:8367492
A:Accession: A47723
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-803 <RUI>
A:Cross-references: UNIPROT:P35447; UNIPARC:UPI000012AC72; GB:L09123; NID:g409244; PIDN:
C:Superfamily: F-spondin: thrombospondin type 1 repeat homology
F:444-455/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:1557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match 10.4%; Score 99; DB 2; Length 803;
Best Local Similarity 26.8%; Pred. No. 0.46;
Matches 38; Conservative 18; Mismatches 64; Indels 22; Gaps 6;

Qy 23 LVQTTMSAGSKTCGMG--ISTRTN-----DNASCRLKQSRICMVRPCE---ADLEEN 72
Db 667 LTEMSEYSECNKSCGKGMIRTRMTPEPGGAVCEPTVORCKRLKCKCKSSGNERRH 726
F:444-455/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:1557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Qy 73 IKKGKCTRTPIKSPKIFELSGCTSMKTYRA-----KFCGCTDGRCTPHRTTTLPEV 127
Db 727 LKQAREKRSKIKEDSDGEGYPCVKKPPWAMWECTKFCGGGIGERMTVYKRRKSSQF 786
F:444-455/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:1557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Qy 128 FKCPDGEVMKKMMFIKTCAH 149
F:444-455/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:1557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR5>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Db 787 TSCKD----KKE---IRACNVH 801

RESULT 13

A47437

LDL receptor-related protein - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: A47437; S27801; T21547

R/Author: J. Greenwald, I.

Proc. Natl. Acad. Sci. U.S.A. 90, 4572-4576, 1993

A/Title: A gene for a low density lipoprotein receptor-related protein in the nematode *C. elegans*

A/Reference number: A47437; PMID:93281621; PMID:8506301

A/Accession: A47437

A/Molecule type: DNA

A/Residues: 1-4753 <Y02>

A/Cross-references: UNIPROT:004833; UNIPARC:UPI000013C4B5; GB:M96150; NID:g156359; PIDN:g156359; PIDN:

A/Note: nucleotide sequence not given; translation not complete in this paper

R/Author: J. Greenwald, I.

Submitted to the EMBL Data Library, July 1992

A/Description: A gene for an LDL receptor-related protein (LPR) in the nematode *C. elegans*

A/Reference number: S27801

A/Accession: S27801

A/Molecule type: DNA

A/Residues: 1-4753 <Y02>

A/Cross-references: UNIPARC:UPI000013C4B5; EMBL:M96150; NID:g156359; PIDN:AAA28105.1; PI

R/Author: J.

Submitted to the EMBL Data Library, June 1996

A/Reference number: Z19439

A/Accession: T21547

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-4753 <W1>

A/Cross-references: UNIPARC:UPI000013C4B5; EMBL:Z73907; PIDN:CAA98124.1; GSPDB:GND00019;

A/Experimental source: clone F29D11

C/Genetics:

A/Map position: 1

A/Introns: 31/1; 88/1; 133/1; 172/3; 219/1; 298/1; 463/2; 526/2; 585/3; 780/2; 874/2; 97

15/1

C/Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding

C/Keywords: tandem repeat; transmembrane protein

F/53-87/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F/92-131/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F/138-175/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F/182-219/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F/223-257/Domain: LDL receptor ligand-binding repeat homology <LDL5>

F/262-297/Domain: LDL receptor ligand-binding repeat homology <LDL6>

F/302-336/Domain: EGF homology <EGF1>

F/1054-1095/Domain: LDL receptor ligand-binding repeat homology <LDL7>

F/1101-1138/Domain: LDL receptor ligand-binding repeat homology <LDL8>

F/1146-1182/Domain: LDL receptor ligand-binding repeat homology <LDL9>

F/1187-1223/Domain: LDL receptor ligand-binding repeat homology <LDL10>

F/1228-1263/Domain: LDL receptor ligand-binding repeat homology <LDL11>

F/1270-1307/Domain: LDL receptor ligand-binding repeat homology <LDL12>

F/1311-1350/Domain: LDL receptor ligand-binding repeat homology <LDL13>

F/1359-1396/Domain: LDL receptor ligand-binding repeat homology <LDL14>

F/1441-1475/Domain: EGF homology <EGF>

F/1611-1654/Domain: LDL receptor YWTD-containing repeat homology <YW33>

F/1792-1829/Domain: LDL receptor ligand-binding repeat homology <LDL15>

F/1834-1868/Domain: LDL receptor ligand-binding repeat homology <LDL16>

F/1874-1912/Domain: LDL receptor ligand-binding repeat homology <LDL17>

F/1919-1956/Domain: LDL receptor ligand-binding repeat homology <LDL18>

F/1961-1997/Domain: LDL receptor ligand-binding repeat homology <LDL19>

F/2006-2044/Domain: LDL receptor ligand-binding repeat homology <LDL20>

F/2049-2093/Domain: LDL receptor ligand-binding repeat homology <LDL21>

F/2100-2145/Domain: LDL receptor ligand-binding repeat homology <LDL22>

F/2140-2184/Domain: LDL receptor ligand-binding repeat homology <LDL23>

F/2187-2232/Domain: LDL receptor ligand-binding repeat homology <LDL24>

F/2236-2283/Domain: EGF homology <EGF1>

F/2327-2366/Domain: LDL receptor ligand-binding repeat homology <LDL25>

F/2367-2405/Domain: LDL receptor ligand-binding repeat homology <LDL26>

F/2409-2446/Domain: LDL receptor ligand-binding repeat homology <LDL27>

F/3753-3788/Domain: LDL receptor ligand-binding repeat homology <LDL28>

F/3793-3830/Domain: LDL receptor ligand-binding repeat homology <LDL29>

F/3833-3871/Domain: LDL receptor ligand-binding repeat homology <LDL30>

F/3878-3912/Domain: LDL receptor ligand-binding repeat homology <LDL31>

F/3917-3951/Domain: LDL receptor ligand-binding repeat homology <LDL32>

F/3959-3995/Domain: LDL receptor ligand-binding repeat homology <LDL33>

F/4000-4040/Domain: LDL receptor ligand-binding repeat homology <LDL34>

F/4049-4083/Domain: LDL receptor ligand-binding repeat homology <LDL35>

F/4092-4130/Domain: EGF homology <EGF2>

F/4343-4386/Domain: LDL receptor YWTD-containing repeat homology <YW38>

Query Match 10.1%; Score 97; DB 1; Length 4753;

Best Local Similarity 21.8%; Pred. No. 3.6;

Matches 46; Conservative 17; Mismatches 68; Indels 80; Gaps 10;

QY 15 PTMIRANLVOTTEMSASCKTGMSITRVNDNASCR---LEKSRICM----- 61

DB 1019 PNELEAKC-----ACRQGFMINKEN-NHSCQKPAKEIKQLCSNSTPOCKN 1065

QY 62 -----VPRCEADLEENIKGKKCI-----RTPKISKPIKPELSGCT 97

DB 1066 GRCLPKEWKCDGENDCLDESDEIDKDKCHETECANTIKCRNTKCIPIAQVCGDDN 1125

QY 98 SMKTYRAKFCGCTDGR---C-----CTPHRTTLPVEFKCP-----DEFWKKNRMF 142

DB 1126 DCGDSDSDVYKCKDQKQKPVCAKKFQCDNR--CIFPMWCKDSNDGCDGSDKLEWCG 1183

QY 143 IKTCAC-----HINCPGDNDIPE 160

DB 1184 NATCAANQFSCAMGRCLPIYWLCDGDNDICYD 1214

RESULT 14

T29247

hypothetical protein F09P9.4 - *Caenorhabditis elegans*

C/Species: *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T29247

R/Author: P. Hawkins, J.

Submitted to the EMBL Data Library, November 1995

A/Description: The sequence of *C. elegans* cosmid F09P9.

A/Reference number: Z20594

A/Accession: T29247

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-654 <MIN>

A/Cross-references: UNIPROT:Q19284; UNIPARC:UPI000007555E; EMBL:U40958; PIDN:AAA81764.1;

C/Genetics:

A/Map position: 4

A/Introns: 89/3; 138/3; 192/3; 260/1; 312/1; 400/2; 445/3; 496/1; 523/1; 558/2; 596/2

Query Match 10.1%; Score 96.5; DB 2; Length 654;

Best Local Similarity 29.2%; Pred. No. 0.63;

Matches 35; Conservative 16; Mismatches 48; Indels 21; Gaps 7;

QY 27 TWSASCKTCGCGISTRVNDNASCRLEKQSLC---WPRCEADLEENIKGKKCIRTP 83

DB 323 SWSASCEFCGSGRQRRVFCNEP--VPRSKYCDGPLETQECTL-----TKC---P 370

QY 84 KISKPIKPELS---GCTSMKTYRAKFCGCTDGRCTPHRTTLPV---EFKCPDGEVWK 138

DB 371 EAMFOSLSTNCSGCG-ALSLASSTFASRRSRMKGQWTLPMDGFKLADPFRIRQ 429

RESULT 15

T14764

hypothetical protein DKFZp434H204.1 - human (fragment)

C/Species: *Homo sapiens* (man)

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T14764

R/Author: R. Hübner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

Submitted to the Protein Sequence Database, August 1999

A/Reference number: Z18181

A;Accession: T14764
 A;Status: Preliminary
 A;Molecule type: mRNA
 A;Residues: 1-898 <MM>
 A;Cross-references: UNIPROT:Q9UFZ4; UNIPARC:UPI00000606B6; EMBL:AL110226
 A;Experimental source: adult testis; clone DKFZp434H204
 C;Genetics:
 A;Note: DKFZp434H204.1

Query Match 10.1%; Score 96.5; DB 2; Length 898;
 Best Local Similarity 28.2%; Pred. No. 0.85;
 Matches 37; Conservative 12; Mismatches 47; Indels 35; Gaps 7;

```

QY 12 GP--DPTMIRANCLVOTTEWAGSCKTCGMG-----ISTRVTNDNASCRLEKOSRLCMV 62
Db 614 GPPADPLVVR-NASWQAGMSECTTCGLGAVWRPVRCSGGRDPCAPAGRPOPARRCHL 672
QY 63 RPCEADLEENIKKGGKCI RTPKISKPIKFELSGCTSMKTYRAKFGVCTDGRCTPHRTT 122
Db 673 RPCATWHSN---WSKCSRS-----CGGSSVRDVQ-----CVDTRDLRPLR-- 711
QY 123 TLVVEFKCPDG 133
Db 712 ----PFHCQPG 718

```

Search completed: January 9, 2006, 11:19:58
 Job time : 41 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rnp) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2006, 11:11:01 ; Search time 160 Seconds

(without alignments)
758.443 Million cell updates/sec

Title: US-09-461-646-4

Perfect score: 956

Sequence: 1 ALAAVRLDTRGPDPPTMIRA.....PGDNDIFPSLYRKYMGDMA 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	956	100.0	275	2	06LCY0 HUMAN
2	956	100.0	349	1	CTGF_HUMAN
3	956	100.0	349	2	06FHL8_HUMAN
4	956	100.0	349	2	05M8T4_HUMAN
5	943	98.6	349	2	097765_PIG
6	938	98.1	349	1	CTGF_BOVIN
7	937	98.0	349	1	CTGF_PIG
8	934	97.7	347	1	CTGF_RAT
9	934	97.7	347	2	053YJ0_RAT
10	934	97.7	348	1	CTGF_MOUSE
11	925	96.8	344	2	098708_CHICK
12	898	93.9	343	2	042607_XENLA
13	898	93.9	343	2	050515_XENLA
14	894	93.5	343	2	05BRN7_XENTR
15	893	93.4	347	2	09PT80_NOTVI
16	838	87.7	345	2	05R133_BRARE
17	802.5	83.9	357	2	04SC24_TETNG
18	692	72.4	125	2	0862T0_BOVIN
19	662	69.2	119	2	0920W6_MOUSE
20	566	69.2	119	2	091V29_MOUSE
21	566	57.3	113	2	092164_RAT
22	547.5	57.3	353	1	NOV_COTJA
23	547.5	57.2	351	1	NOV_CHICK
24	524.5	54.9	343	1	NOV_XENLA
25	524.5	54.9	343	2	061NN3_XENLA
26	519.5	54.3	354	1	NOV_MOUSE
27	519	54.3	357	1	NOV_HUMAN
28	518.5	54.2	357	2	061S33_HUMAN
29	506	52.9	351	1	NOV_RAT
30	499	52.2	375	2	098TX5_XENLA
31	498	52.1	375	2	05BL74_XENTR

32	489.5	51.2	379	1	CTR61_RAT	096872	rattus norv
33	488.5	51.1	361	2	04RJ65_TETNG	04169	tetradon n
34	487.5	51.0	379	1	CTR61_MOUSE	P18406	mus muscicu
35	487.5	51.0	379	2	09WTM9_RAT	09wtm9	rattus norv
36	487.5	51.0	379	2	066HT5_RAT	066ht5	rattus norv
37	485.5	50.8	381	1	CTR61_HUMAN	000622	homo sapien
38	485.5	50.8	381	1	06F18_HUMAN	06f18	homo sapien
39	479.5	50.2	375	1	CEP10_CHICK	P19336	gallus gall
40	478	50.0	359	2	04ZJF1_CHICK	04zjf1	gallus gall
41	473.5	49.5	381	2	053FA4_HUMAN	053fa4	homo sapien
42	461	48.2	385	2	061R79_XENLA	061r79	xenopus lae
43	459	48.0	369	2	06NMA0_BRARE	06nma0	brachydanto
44	459	48.0	400	2	06F12_BRARE	06f12	brachydanto
45	445	46.5	318	2	04SH80_TETNG	04sh80	tetradon n

ALIGNMENTS

RESULT 1
06LCY0 HUMAN PRELIMINARY; PRT; 275 AA.
ID 06LCY0;
AC 06LCY0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Connective tissue growth factor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92022597; PubMed=1925598;
RA Sutter T.R., Guzman K., Doid K.M., Greenlee W.F.;
RT "Targets for dioxin: genes for plasmidogen activator inhibitor-2 and
interleukin-1 beta."
RL Science 254:415-418(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91373462; PubMed=1654338; DOI=10.1083/jcb.114.6.1285;
RA Bradham D.M., Igarashi A., Potter R.L., Groendorst G.R.;
RT "Connective tissue growth factor: a cysteine-rich mitogen secreted by
human vascular endothelial cells is related to the SRC-induced
immediate early gene product CEF-10."
RL J. Cell Biol. 114:1285-1294(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Cody C.W., Walker N.J., Greenlee W.F., Sutter T.R.;
RT Submitted (SEP-1994) to the EMBL/Genbank/DBJ databases.
RL EMBL; U14750; AAA75378.1; -; mRNA.
GO GO:0005576; C:extracellular region; IEA.
GO GO:0005520; F:insulin-like growth factor binding; IEA.
GO GO:0001558; P:regulation of cell growth; IEA.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR000867; Insl_gro_fac_pr.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PR00007; Cys_knot_1.
DR Pfam; PR00219; IGFBP_1.
DR Pfam; PR00090; TSP_1; 1.
DR Pfam; PR00093; VWC_1; 1.
DR SMART; SM00041; CT_1.
DR SMART; SM00209; TSP1_1.
DR SMART; SM00214; VWC_1.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00992; TSP1_1.
DR PROSITE; PS01208; VWF_C_1; 1.
DR PROSITE; PS0184; VWF_C_2; 1.
FT NON_TER 1 1

SEQUENCE 275 AA; 30476 MW; 332D31C6P4380815 CRC64;
Query Match 100.0%; Score 956; DB 2; Length 275;
Beet Local Similarity 100.0%; Pred. No. 4,4e-81;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ALAAVRLEDTPGPPPTMIRANCLVOTTEWSACSKTCGWSIGSTRVYNDNASCRLEKOSRLC 60
DB 104 ALAAVRLEDTPGPPPTMIRANCLVOTTEWSACSKTCGWSIGSTRVYNDNASCRLEKOSRLC 163
OY 61 MVRPEADLEENIKKKKICRTPKISKPIKELSGCTSMKTYRAFCGVCCTDGRCTPHR 120
DB 164 MVRPEADLEENIKKKKICRTPKISKPIKELSGCTSMKTYRAFCGVCCTDGRCTPHR 223
OY 121 TTTTPVERKCPDGEPMKKNMFITKTCACHYNCPGNDIFESLYYRXKYGMA 172
DB 224 TTTTPVERKCPDGEPMKKNMFITKTCACHYNCPGNDIFESLYYRXKYGMA 275
RESULT 2
CTGF HUMAN STANDARD; PRT; 349 AA.
AC P23279; Q960X2;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Connective tissue growth factor precursor (Hypertrophic chondrocyte-specific protein 24).
GN Name=CTGF; Synonyms=CCN2, HCS24;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=umbilical vein endothelial cell;
MEDLINE=91373462; PubMed=1654338; DOI=10.1083/jcb.114.6.1285;
RA Bradham D.M., Igarashi A., Potter R.L., Greendörst G.R.;
RT "Connective tissue growth factor: a cysteine-rich mitogen secreted by human vascular endothelial cells is related to the SRC-induced
RT immediate early gene product CBF-10.";
RT J. Cell Biol. 114:1285-1294(1991).
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=umbilical vein endothelial cell;
MEDLINE=93187114; PubMed=1293144;
RA Igarashi A., Bradham D.M., Okochi H., Grotenhorst G.R.;
RT "Connective tissue growth factor.";
RT J. Dermatol. 19:642-643(1992).
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta;
MEDLINE=97207446; PubMed=9054739;
RA Oemar B.S., Werner A., Garner T.F.;
RT "Human connective tissue growth factor is expressed in advanced
RT atherosclerotic lesions.";
RT Circulation 95:831-839(1997).
RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RA Li Q.-H., Wang L.-C., Liu L.-D., Dong S.-Z., Wang J.-J., Hu F.,
RA Wang J., He S.-Q., Dong C.-H., Zhao S.-D., Zhao H.-L.;
RT "Expression, purification and bio-activity of human connective tissue
RT growth factor.";
RT Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RA Dai W.-J., Jiang H.-C., Fu S.-B.;
RT "Complete mRNA sequence of human connective tissue growth factor.";
RT Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RA Kainane N., Chen X., Rolle A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Pielan M., Farmer A.;
RT "Cloning of human full-length cDNA in BD Creator(TM) system donor
RT vector.";
RT Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RA Halleck A., Ebert L., Koundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry
RT vector (pDONR201).";
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
RA Wilmink L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Alincough R.,
RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
RA Babbage A.K., Beggsley C.L., Bailey J., Banerjee R., Barker D.J.,
RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
RA Cullier K.M., Dhani P., Davies J., Dunn M., Earthowl M.E.,
RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
RA Fraynkland J., French L., Garner P., Garnett J., Ghori M.J.,
RA Gilby L.M., Gillson C.J., Gilthorpe R.J., Grafham D.V., Grant M.,
RA Griddle S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcott R.,
RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA Lawlor S., Leonamontler D.A., Leverisha M., Lloyd C.R., Lloyd D.M.,
RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
RA Maalen G.L., Matthews L., McCann O.T., McLaren S.J., McRay K.,
RA McMuray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
RA Newk K.L., Oliver K., Overton-Larby E.K., Parker A., Patel R.,
RA Pearce A.V., Peck A.I., Phillips B.J.C.T., Phillips S., Plumb R.W.,
RA Porter K.M., Ramsey Y., Randy S.A., Rice C.M., Ross M.T., Seale S.M.,
RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith G., Teeter J.,
RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Teeter J.,
RA Theaker A.J., Thomas D.W., Thorne A., Tracey A., Tromans A., Tubby B.,
RA Wall M., Wallis J.W., West A.P., White S.S., Whitehead S.L.,
RA Whitaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
RT "The DNA sequence and analysis of human chromosome 6.";
RT Nature 425:805-811(2003).
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Chondrocyte;
MEDLINE=20080284; PubMed=10614647; DOI=10.1210/en.141.1.264;
RA Nakamishi T., Nishida T., Shimo T., Kobayashi K., Kubo T.,
RA Tanakani T., Tezuka K., Takigawa M.;
RT "Effects of CTGF/Hcs24, a product of a hypertrophic chondrocyte-specific gene, on the proliferation and differentiation of
RT chondrocytes in culture.";
RT Endocrinology 141:264-273(2000).
RN HEPARIN-BINDING, AND CELL ADHESION.
RP MEDLINE=22442376; PubMed=12553878; DOI=10.1677/joe.0.176R001;
RA Ball D.K., Rachfal A.W., Kemper S.A., Briggs D.R.;
RT "The heparin-binding 10 kDa fragment of connective tissue growth
RT factor (CTGF) containing module 4 alone stimulates cell adhesion.";
RT J. Endocrinol. 176:R1-R7(2003).
RN -1- FUNCTION: Major connective tissue mitogen secreted by
CC vascular endothelial cells. Promotes proliferation and
CC differentiation of chondrocytes. Mediates heparin- and divalent

Oy 61 MVRPEADLEBNIKKGGKCIIRTPKISKIPKELSGCTSMKTYRAKFCGVCCTDGRCTPBR 120
Db 238 MVRPEADLEBNIKKGGKCIIRTPKISKIPKELSGCTSMKTYRAKFCGVCCTDGRCTPBR 297
Oy 121 TTTTLPVEFKCPDGEVWKKMMFMFKTCACHYNCPGNDIFESLYYRKMYGDMA 172
Db 298 TTTTLPVEFKCPDGEVWKKMMFMFKTCACHYNCPGNDIFESLYYRKMYGDMA 349

RESULT 4

OSM874_HUMAN
ID OSM874_HUMAN PRELIMINARY; PRT; 349 AA.
AC OSM874;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Connective tissue growth factor.
GN Name=CTGF;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Peripheral Nervous System;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426039999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheffen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RA Director MGC Project;
RL Submitted (DEC-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL, BC087839; AAH87839.1; -; mRNA.
SQ SEQUENCE 349 AA; 38069 MW; 0ECF8470B357BA95 CRC64;

Query Match 100.0%; Score 956; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 5,66-81;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ALAAVRLBDTFFGPDPTMIRANCLVQTTWWSACSKTCGMSITRVYNDNASCRLEKQSRILC 60
Db 178 ALAAVRLBDTFFGPDPTMIRANCLVQTTWWSACSKTCGMSITRVYNDNASCRLEKQSRILC 237
Oy 61 MVRPEADLEBNIKKGGKCIIRTPKISKIPKELSGCTSMKTYRAKFCGVCCTDGRCTPBR 120
Db 238 MVRPEADLEBNIKKGGKCIIRTPKISKIPKELSGCTSMKTYRAKFCGVCCTDGRCTPBR 297
Oy 121 TTTTLPVEFKCPDGEVWKKMMFMFKTCACHYNCPGNDIFESLYYRKMYGDMA 172
Db 298 TTTTLPVEFKCPDGEVWKKMMFMFKTCACHYNCPGNDIFESLYYRKMYGDMA 349

RESULT 5

O97765_PIG
ID O97765_PIG PRELIMINARY; PRT; 349 AA.
AC O97765;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Connective tissue growth factor.
GN Name=CTGF;
OS Sus scrofa (Pig);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sus.
NCBI_TaxID=9823;
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Uterus;
RA Harding P.A., Brigstock D.R.,
RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL, U70060; AAD00174.1; -; mRNA.
DR GO:0005576; C:extracellular region; IEA.
DR GO:0005520; F:insulin-like growth factor binding; IEA.
DR GO:0001558; P:regulation of cell growth; IEA.
DR InterPro: IPR006208; Cys_knot.
DR InterPro: IPR006207; Cys_knot_C.
DR InterPro: IPR000867; Insl_gro_fac_pr.
DR InterPro: IPR001007; WVF_C.
DR Pfam: PF00007; Cys_knot_1.
DR Pfam: PF00219; IGFBR; 1.
DR Pfam: PF00090; TSP_1; 1.
DR Pfam: PF00093; WVC; 1.
DR SMART: SM00041; CT; 1.
DR SMART: SM00121; IB; 1.
DR SMART: SM00209; TSP; 1.
DR SMART: SM00214; WVC; 1.
DR PROSITE: PS01185; CTCK_1; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS00222; IGF_BINDING; 1.
DR PROSITE: PS00992; TSP; 1.
DR PROSITE: PS01208; WVF_C; 1.
DR PROSITE: PS0184; WVF_C_2; 1.
SQ SEQUENCE 349 AA; 37946 MW; 35AB4275AC1D4B3A CRC64;

Query Match 98.6%; Score 943; DB 2; Length 349;
Best Local Similarity 97.7%; Pred. No. 9,16-80;
Matches 168; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ALAAVRLBDTFFGPDPTMIRANCLVQTTWWSACSKTCGMSITRVYNDNASCRLEKQSRILC 60
Db 178 ALAAVRLBDTFFGPDPTMIRANCLVQTTWWSACSKTCGMSITRVYNDNASCRLEKQSRILC 237
Oy 61 MVRPEADLEBNIKKGGKCIIRTPKISKIPKELSGCTSMKTYRAKFCGVCCTDGRCTPBR 120
Db 238 MVRPEADLEBNIKKGGKCIIRTPKISKIPKELSGCTSMKTYRAKFCGVCCTDGRCTPBR 297
Oy 121 TTTTLPVEFKCPDGEVWKKMMFMFKTCACHYNCPGNDIFESLYYRKMYGDMA 172
Db 298 TTTTLPVEFKCPDGEVWKKMMFMFKTCACHYNCPGNDIFESLYYRKMYGDMA 349

RESULT 6

CTGF_BOVIN
ID CTGF_BOVIN STANDARD; PRT; 349 AA.
AC O18739; O8GL71;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Connective tissue growth factor precursor.
GN Name=CTGF; Synonyms=CN2;
OS Bos taurus (Bovine);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.

CC NCBI_TaxId=9913;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Arteria;
 RA Lilienfeld B., Lin Z., Fotakis T., Schimanski M., Biehn A.,
 RA Kautz M., Kauffmann G., Schweigerer U., Ziegler R., Nawroth P.P.;
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBD databases.
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Liver;
 RA Mathae M., Schwilters C., Hove M., Rupp S., Erond N.E.;
 RT "Bovine connective tissue growth factor, organization of the
 RT chromosomal gene and demonstration of promoter activity.";
 RL Submitted (Sep-2000) to the EMBL/GenBank/DBD databases.
 CC -1- FUNCTION: Major connective tissue microattractant secreted by
 CC and differentiation of chondrocytes (By similarity). Mediates heparin-
 CC and divalent cation-dependent cell adhesion in many cell types
 CC including fibroblasts, myofibroblasts, endothelial and epithelial
 CC cells (By similarity). Enhances fibroblast growth factor-induced
 CC DNA synthesis (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Found in the extracellular matrix and as a
 CC soluble form (By similarity).
 CC -1- SIMILARITY: Belongs to the CCN family.
 CC -1- SIMILARITY: Contains 1 CTCK (C-terminal cysteine knot-like) domain.
 CC -1- SIMILARITY: Contains 1 IGFBP domain.
 CC -1- SIMILARITY: Contains 1 TSP type-1 domain.
 CC -1- SIMILARITY: Contains 1 VMFC domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL AF00137, AAB6596.1; -, mRNA.
 DR EMBL AF009555, AAG30290.1; -, Genomic DNA.
 DR InterPro: IPR006208; Cys_knot.
 DR InterPro: IPR006207; Cys_knot_C.
 DR InterPro: IPR012395; IGFBP_CNN.
 DR InterPro: IPR000867; IGFBP_like.
 DR InterPro: IPR000864; TSP1.
 DR InterPro: IPR01007; VMF_C.
 DR Pfam: PF00007; Cys_knot; 1.
 DR Pfam: PF00219; IGFBP; 1.
 DR Pfam: PF00090; TSP1; 1.
 DR Pfam: PF00093; VMCF; 1.
 DR PIRSF: PIRSF036495; IGFBP_rP_CNN; 1.
 DR SMART: SMART0041; CT; 1.
 DR SMART: SMART0041; IB; 1.
 DR SMART: SMART00209; TSP1; 1.
 DR SMART: SMART00214; VMCF; 1.
 DR PROSITE: PS0185; CTCK_1; 1.
 DR PROSITE: PS01225; CTCK_2; 1.
 DR PROSITE: PS00222; IGF_BINDING; 1.
 DR PROSITE: PS00922; TSP1; 1.
 DR PROSITE: PS01208; VMFC_1; 1.
 DR PROSITE: PS01084; VMFC_2; 1.
 KW Cell adhesion; DNA synthesis; Extracellular matrix; Heparin-binding;
 KW Signal.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 349 Connective tissue growth factor.
 FT DOMAIN 33 100 IGFBP.
 FT DOMAIN 101 167 VMFC.
 FT DOMAIN 198 243 TSP type-1.
 FT DOMAIN 256 330 CTCK.
 FT REGION 247 349 Heparin-binding (By similarity).
 FT DISUFID 256 293 By similarity.
 FT DISUFID 273 307 By similarity.
 FT DISUFID 287 325 By similarity.
 FT DISUFID 292 329 By similarity.
 FT CONFLICT 28 28 D -> DC (in Ref. 1).

FT CONFLICT 58 58 Missing (in Ref. 1).
 FT CONFLICT 88 88 A -> T (in Ref. 1).
 FT CONFLICT 103 104 CV -> YI (in Ref. 1).
 FT CONFLICT 166 169 CDEP -> SRDE (in Ref. 1).
 FT CONFLICT 184 184 P -> L (in Ref. 1).
 FT CONFLICT 200 200 L -> Q (in Ref. 1).
 FT CONFLICT 209 209 C -> Y (in Ref. 1).
 FT CONFLICT 269 269 E -> Q (in Ref. 1).
 FT CONFLICT 284 284 C -> F (in Ref. 1).
 SQ SEQUENCE 349 AA; 37924 MW; 5FEC8E83EFBAF99 CRC64;
 Query Match 98.1%; Score 938; DB 1; Length 349;
 Best Local Similarity 98.3%; Pred. No. 2.7e-79;
 Matches 169; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ALAAYRLDPTGPDPTMRANCLVOTTEMSACKTCGNGISIRYNNDAACGLEKOSRLC 60
 DB 178 ALAAYRPEDTFGPDPTMRANCLVOTTEMSACKTCGNGISIRYNNDAACGLEKOSRLC 237
 QY 61 MYRPEADLEENIKKGGKICIRPKISKPIKPELGGCTSKTYRAKFCGCTDGRCTPPR 120
 DB 238 MYRPEADLEENIKKGGKICIRPKISKPIKPELGGCTSKTYRAKFCGCTDGRCTPPR 297
 QY 121 TTTLPEVFKCPDGEVWKKMMFIRKTCACHYNGPDNDIFESLYYRMYGDMA 172
 DB 298 TTTLPEVFKCPDGEVWKKMMFIRKTCACHYNGPDNDIFESLYYRMYGDMA 349
 RESULT 7
 CTGF_PIG STANDARD; PRT; 349 AA.
 ID CTGF_PIG
 AC 019113;
 DT 15-JUL-1998 (rel. 36, Created)
 DT 15-JUL-1998 (rel. 36, Last sequence update)
 DT 10-MAY-2005 (rel. 47, Last annotation update)
 DE Connective tissue growth factor precursor.
 GN Name=CTGF; Synonyms=CCN2;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
 OC Sus.
 OC NCBI_TaxId=9823;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Uterus;
 RX MEDLINE=97390475; PubMed=9242708; DOI=10.1074/jbc.272.32.20275;
 RA Brigstock D.R., Steffen C.L., Kim G.Y., Vegunta R.K., Diehl J.R.,
 RA Harding P.A.;
 RT "Purification and characterization of novel heparin-binding growth
 RT factors in uterine secretory fluids. Identification as heparin-
 RT regulated Mr 10,000 forms of connective tissue growth factor.";
 RL J. Biol. Chem. 272:20275-20282(1997).
 CC -1- FUNCTION: Major connective tissue microattractant secreted by
 CC and differentiation of chondrocytes (By similarity). Mediates heparin-
 CC and divalent cation-dependent cell adhesion in many cell types
 CC including fibroblasts, myofibroblasts, endothelial and epithelial
 CC cells (By similarity). Enhances fibroblast growth factor-induced
 CC DNA synthesis (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Found in the extracellular matrix and as a
 CC soluble form (By similarity).
 CC -1- SIMILARITY: Belongs to the CCN family.
 CC -1- SIMILARITY: Contains 1 CTCK (C-terminal cysteine knot-like) domain.
 CC -1- SIMILARITY: Contains 1 IGFBP domain.
 CC -1- SIMILARITY: Contains 1 TSP type-1 domain.
 CC -1- SIMILARITY: Contains 1 VMFC domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; U83916; AAC48756.1; -; mRNA.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR012395; IGFBP_CNN.
DR InterPro; IPR000867; IGFBP_like.
DR InterPro; IPR000884; TSPL.
DR InterPro; IPR001007; WVF_C.
DR Pfam; PF00007; Cys_knot_1.
DR Pfam; PF00219; IGFBP_1.
DR Pfam; PF00090; TSP_1; 1.
DR Pfam; PF00093; WVC; 1.
DR PIRSF; PIRSF036495; IGFBP_rp_CNN; 1.
DR SMART; SM00041; CT; 1.
DR SMART; SM00121; IB; 1.
DR SMART; SM00209; TSPL; 1.
DR SMART; SM00214; WVC; 1.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00222; IGF_BINDING; 1.
DR PROSITE; PS50092; TSPL_1.
DR PROSITE; PS01208; WVFC_1; 1.
DR PROSITE; PS50184; WVFC_2; 1.
KW Cell adhesion; DNA synthesis; Extracellular matrix; Heparin-binding;
KW Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 349 Connective tissue growth factor.
FT DOMAIN 33 100 IGFBP.
FT DOMAIN 101 167 WVFC.
FT DOMAIN 198 243 TSP type-1.
FT DOMAIN 256 330 CTCK.
FT REGION 247 349 Heparin-binding (By similarity).
FT DISULFID 256 293 By similarity.
FT DISULFID 273 307 By similarity.
FT DISULFID 284 323 By similarity.
FT DISULFID 287 325 By similarity.
FT DISULFID 292 329 By similarity.
SQ SEQUENCE 349 AA; 38007 MW; BBS10B2B52D4A0 CRC64;

Query Match 98.0%; Score 937; DB 1; Length 349;
Best Local Similarity 97.1%; Pred. No. 3.3e-79;
Matches 167; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALAARLDTEGPDPTMIRANCLVOTTEMSACSKTCGNGISIRVYNDNASCRLKQSLC 60
DB 178 ALAARLDTEGPDPTMIRANCLVOTTEMSACSKTCGNGISIRVYNDNASCRLKQSLC 237
QY 61 MVRPEADLEENIKKGGKCIIRTPKISKPIKPELSGCTSMKTYRAKFCGCTDGRCTPHR 120
DB 238 MVRPEADLEENIKKGGKCIIRTPKISKPIKPELSGCTSMKTYRAKFCGCTDGRCTPHR 297
QY 121 TTTTLEVERKCPDGEVWKKMMFMKTCACHYNCPSGNDIFESLYYKKTGDMA 172
DB 298 TTTTLEVERKCPDGEVWKKMMFMKTCACHYNCPSGNDIFESLYYKKTGDMA 349

RESULT 8
CTGF_RAT STANDARD; PRT; 347 AA.
AC Q9RIE9; Q9WVS1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Connective tissue growth factor precursor.
GN Name=CTGF; Synonym=Ccn2;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20145935; PubMed=10679821;
RX

RX DOI=10.1002/(SICI)1097-4644(20000401)77:1<103::AID-OCB11>3.0.CO;2-G;
RA Xu J., Smock S.L., Safadi F.F., Rosenzweig A.B., Odgren P.R.,
RA Marks S.C., Jr., Owen T.A., Popoff S.N.;
RT "Cloning the full-length cDNA for rat connective tissue growth factor:
RT implications for skeletal development.";
RL J. Cell. Biochem. 77:103-115(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tezuka K., Tamatani T.;
RT "Rattus norvegicus connective tissue growth factor.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Major connective tissue mitotactant secreted by
CC vascular endothelial cells. Promotes proliferation and
CC differentiation of chondrocytes (By similarity). Mediates heparin-
CC and divalent cation-dependent cell adhesion in many cell types
CC including fibroblasts, myofibroblasts, endothelial and epithelial
CC cells (By similarity). Enhances fibroblast growth factor-induced
CC DNA synthesis (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the CN family.
CC -1- SIMILARITY: Contains 1 CTCK (C-terminal cysteine knot-like) domain.
CC -1- SIMILARITY: Contains 1 IGFBP domain.
CC -1- SIMILARITY: Contains 1 TSP type-1 domain.
CC -1- SIMILARITY: Contains 1 WVFC domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AF120275; AAD39132.1; -; mRNA.
CC EMBL; AB023068; BAA82125.1; -; mRNA.
CC Ensembl; ENSRNCG00000015036; Rattus norvegicus.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR012395; IGFBP_CNN.
DR InterPro; IPR000867; IGFBP_like.
DR InterPro; IPR000884; TSPL.
DR InterPro; IPR001007; WVF_C.
DR Pfam; PF00007; Cys_knot_1.
DR Pfam; PF00219; IGFBP_1.
DR Pfam; PF00090; TSP_1; 1.
DR Pfam; PF00093; WVC; 1.
DR PIRSF; PIRSF036495; IGFBP_rp_CNN; 1.
DR SMART; SM00041; CT; 1.
DR SMART; SM00121; IB; 1.
DR SMART; SM00209; TSPL; 1.
DR SMART; SM00214; WVC; 1.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00222; IGF_BINDING; 1.
DR PROSITE; PS50092; TSPL_1.
DR PROSITE; PS01208; WVFC_1; 1.
DR PROSITE; PS50184; WVFC_2; 1.
KW Cell adhesion; DNA synthesis; Extracellular matrix; Heparin-binding;
KW Signal.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 347 Connective tissue growth factor.
FT DOMAIN 31 98 IGFBP.
FT DOMAIN 99 165 WVFC.
FT DOMAIN 196 241 TSP type-1.
FT DOMAIN 254 328 CTCK.
FT REGION 245 347 Heparin-binding (By similarity).
FT DISULFID 254 291 By similarity.
FT DISULFID 271 305 By similarity.
FT DISULFID 282 321 By similarity.
FT DISULFID 285 323 By similarity.
FT DISULFID 290 327 By similarity.
FT CONFLICT 35 35 A -> R (in Ref. 2).
FT CONFLICT 94 94 T -> P (in Ref. 2).
SQ SEQUENCE 347 AA; 37756 MW; CFBETA1976B7B16 CRC64;


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Query Match          97.7%; Score 934; DB 1; Length 347;
Best Local Similarity 95.9%; Pred. No. 6,3e-79;
Matches 165; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAARLRLDTPGDPPTMIRANCLVQTTWSACSKTCGMGISTRTVNDNASCRLEKQSRIC 60
DB 176 ALAARLRLDTPGDPPTMIRANCLVQTTWSACSKTCGMGISTRTVNDNTPCRLKQSRIC 235
QY 61 MYRPEADLEENIKKGGKICIRTPKISKPIKEFLSGCTSMKTYRAFCGYCTDGRCTPPR 120
DB 236 MYRPEADLEENIKKGGKICIRTPKIAKPYKPELSCGTSVKTYPRAFCGYCTDGRCTPPR 295
QY 121 TTTLPEVEKCPDGEVKKMMFMFKTCACHYNCRGNDIPESLYYRMYGDM 172
DB 296 TTTLPEVEKCPDGEVKKMMFMFKTCACHYNCRGNDIPESLYYRMYGDM 347

RESULT 9
Q53YJ0 RAT PRELIMINARY; PRT; 347 AA.
ID 053YJ0;
AC 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
OS Connective tissue growth related protein.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Miscar;
RA Ma L.N., Zou Y.L.;
RT "Connective Tissue Growth Related Gene.";
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF596447; AAT08023.1; -; -; CFE81A19766B7B16 CRC64;
SQ SEQUENCE 347 AA; 37756 MW; 19766B7B16 CRC64;

Query Match          97.7%; Score 934; DB 2; Length 347;
Best Local Similarity 95.9%; Pred. No. 6,3e-79;
Matches 165; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALAAYRLBDTPGDPPTMIRANCLVQTTWSACSKTCGMGISTRTVNDNASCRLEKQSRIC 60
DB 176 ALAAYRLBDTPGDPPTMIRANCLVQTTWSACSKTCGMGISTRTVNDNTPCRLKQSRIC 235
QY 61 MYRPEADLEENIKKGGKICIRTPKISKPIKEFLSGCTSMKTYRAFCGYCTDGRCTPPR 120
DB 236 MYRPEADLEENIKKGGKICIRTPKIAKPYKPELSCGTSVKTYPRAFCGYCTDGRCTPPR 295
QY 121 TTTLPEVEKCPDGEVKKMMFMFKTCACHYNCRGNDIPESLYYRMYGDM 172
DB 296 TTTLPEVEKCPDGEVKKMMFMFKTCACHYNCRGNDIPESLYYRMYGDM 347

RESULT 10
CTGF_MOUSE
ID CTGF_MOUSE STANDARD; PRT; 348 AA.
AC F29268; 0922U0;
DT 01-DEC-1992 (Rel. 24, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Connective tissue growth factor precursor (FISP-12 protein)
DE (Hypertrophic chondrocyte-specific protein 24).
GN Name=Ctgf; Synonym=Ccm2, Fisp-12, Fisp12, Hcc24;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

RX MEDLINE=91363290; PubMed=1888698;
RA Rybeck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;
RT "Structure, mapping, and expression of fisp-12, a growth factor-
inducible gene encoding a secreted cysteine-rich protein.";
RL Cell Growth Differ. 2:225-233(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91229699; PubMed=2029337;
RA Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;
RT "Identification of a gene family regulated by transforming growth
factor-beta.";
RL DNA Cell Biol. 10:293-300(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strusberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherbenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=97327410; PubMed=9184077; DOI=10.1006/excr.1997.3548;
RA Kireeva M.L., Latinkic B.V., Kolesnikova T.V., Chen C.-C., Yang G.P.,
RA Abler A.S., Lau L.F.;
RT "Cyf1 and Fisp12 are both ECM-associated signaling molecules;
activities, metabolism, and localization during development.";
RL Exp. Cell Res. 233:63-77(1997).
RN [5]
RP FUNCTION.
RX MEDLINE=99182484; PubMed=10082563;
RA Babic A.M., Chen C.-C., Lau L.F.;
RT "Fisp12/mouse connective tissue growth factor mediates endothelial
cell adhesion and migration through integrin alphavbeta3, promotes
endothelial cell survival, and induces angiogenesis in vivo.";
RL Mol. Cell. Biol. 19:2958-2966(1999).
CC -1- FUNCTION: Major connective tissue microattractant secreted by
CC vascular endothelial cells. Promotes proliferation and
CC differentiation of chondrocytes (By similarity). Mediates heparin-
CC and divalent cation-dependent cell adhesion in many cell types
CC including fibroblasts, myofibroblasts, endothelial and epithelial
CC cells (By similarity). Enhances fibroblast growth factor-induced
CC DNA synthesis (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Found in the extracellular matrix and as a
CC soluble form.
CC -1- TISSUE SPECIFICITY: Testis, spleen, kidney, lung, heart, and brain
CC (lowest level in testis and highest in lung).
CC -1- INDUCTION: By growth factors.
CC -1- SIMILARITY: Belongs to the CCN family.
CC -1- SIMILARITY: Contains 1 CTCK (C-terminal cysteine knot-like) domain.
CC -1- SIMILARITY: Contains 1 IGFBP domain.
CC -1- SIMILARITY: Contains 1 TSP type-1 domain.
CC -1- SIMILARITY: Contains 1 WFC domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

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CC use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC EMBL; M70641; AAA37627.1; -; Genomic_DNA.
CC EMBL; M70642; AAA37628.1; -; mRNA.
CC EMBL; M80263; AAA73135.1; -; mRNA.
CC EMBL; BC006783; AAH06783.1; -; mRNA.
CC PIR; A40578; A40578.
CC Ensemble; ENSMUSG0000001997; Mus musculus.
DR MGI; MGI.95537; Ctgf.
DR GO; GO:0005578; C:extracellular matrix (seu Metazoa); IDA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008201; F:heparin binding; IDA.
DR GO; GO:0005178; F:integrin binding; IDA.
DR GO; GO:0001525; P:angiogenesis; IDA.
DR GO; GO:0001502; P:cell differentiation; IDA.
DR GO; GO:0030154; P:cell migration; IDA.
DR GO; GO:0016477; P:cell migration; IDA.
DR GO; GO:0007160; P:cell-matrix adhesion; IDA.
DR GO; GO:0008543; P:fibroblast growth factor receptor signaling. . .; IDA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IDA.
DR GO; GO:0001503; P:osteification; IMP.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR012395; IGFBP_CNN.
DR InterPro; IPR000867; IGFBP_like.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF00007; Cys_knot; 1.
DR Pfam; PF00219; IGFBP; 1.
DR Pfam; PF00090; TSP_1; 1.
DR Pfam; PF00093; VWC; 1.
DR PIRSF; PIRSF036495; IGFBP_rp_CNN; 1.
DR SMART; SM00041; CT; 1.
DR SMART; SM00121; IB; 1.
DR SMART; SM00209; TSP1; 1.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00222; IGF_BINDING; 1.
DR PROSITE; PS50092; TSP1; 1.
DR PROSITE; PS01208; VWF_C_1; 1.
DR PROSITE; PS50184; VWF_C_2; 1.
KW Cell adhesion; DNA synthesis; Extracellular matrix; Heparin-binding;
KW Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 348 Connective tissue growth factor.
FT DOMAIN 32 99 IGFBP.
FT DOMAIN 100 166 VWF.
FT DOMAIN 197 242 TSP type-1.
FT DOMAIN 255 329 CTCK.
FT REGION 246 348 Heparin-binding (by similarity).
FT DISULFID 255 292 By similarity.
FT DISULFID 272 306 By similarity.
FT DISULFID 283 322 By similarity.
FT DISULFID 286 324 By similarity.
FT DISULFID 291 328 By similarity.
FT CONFLICT 161 161 E -> K (in Ref. 1).
SQ SEQUENCE 348 AA; 37794 MW; 4D7B6D9089174049 CRC64;
Query Match 97.7%; Score 934; DB 1; Length 348;
Best Local Similarity 95.9%; Pred. No. 6.3e-79;
Matches 165; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

DB 297 TTTLPVEFKCPDGEVVKIKMMFIKTCACHYNCBGNDIFESLYYKMYGDMA 348
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RESULT 11
Q98T08_CHICK PRELIMINARY; PRT; 344 AA.
ID Q98T08
AC Q98T08
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Connective tissue growth factor precursor (Connective tissue growth
DE factor/hypertrophic chondrocyte-specific protein 24).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22559415; PubMed=12674494; DOI=10.1515/BC.2003.001;
RA Mukudai Y., Kubota S., Takigawa M.;
RT "Conserved repressive regulation of connective tissue growth
RT factor/hypertrophic chondrocyte-specific gene 24 (ctgf/hcs24) enabled
RT by different elements and factors among vertebrate species.";
RL Biol. Chem. 384:1-9(2003).
RL EMBL; AJ298335; CAC33438.1; -; mRNA.
DR EMBL; AF463317; AL46834.1; -; mRNA.
DR Ensemble; ENSGALG00000002909; Gallus gallus.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0005520; F:insulin-like growth factor binding; IEA.
DR GO; GO:0001558; P:regulation of cell growth; IEA.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR000867; Insl_gro_fac_pr.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF00007; Cys_knot; 1.
DR Pfam; PF00219; IGFBP; 1.
DR Pfam; PF00090; TSP_1; 1.
DR Pfam; PF00093; VWC; 1.
DR SMART; SM00041; CT; 1.
DR SMART; SM00121; IB; 1.
DR SMART; SM00209; TSP1; 1.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00222; IGF_BINDING; 1.
DR PROSITE; PS50092; TSP1; 1.
DR PROSITE; PS01208; VWF_C_1; 1.
DR PROSITE; PS50184; VWF_C_2; 1.
KW Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 344 connective tissue growth factor.
SQ SEQUENCE 344 AA; 37499 MW; 69B639AF9B1D00 CRC64;
Query Match 96.8%; Score 925; DB 2; Length 344;
Best Local Similarity 95.3%; Pred. No. 4.3e-76;
Matches 164; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 61 MVRPCADLEENIKKKKICITPTKISKIPKELSGCTSMKTYRAKFCGVCITDGRCTPHR 120
DB 233 MVRPCADLEENIKKKKICITPTKISKIPKELSGCTSMKTYRAKFCGVCITDGRCTPHR 292
QY 121 TATLPVEFKCPDGEVMMKMMFIKTCACHYNCPGNDIFESLYRYKMYGDMA 172
DB 293 TATLPVEFKCPDGEVMMKMMFIKTCACHYNCPGNDIFESLYRYKMYGDMA 344

RESULT 12

ID 042607_XENLA PRELIMINARY; PRT; 343 AA.
AC 042607;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Connective tissue growth factor XCTGF.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8335;
RX NUCLEOTIDE SEQUENCE.
RP ying Z., King M.L.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U43524; AAB67639.1; -; mRNA.
DR EMBL; U43523; AAB67638.1; -; Genomic DNA.
DR GO; GO:0005576; C; Extracellular region; IEA.
DR GO; GO:0008083; F; Growth factor activity; IEA.
DR GO; GO:0005520; F; Insulin-like growth factor binding; IEA.
DR GO; GO:0001558; P; Regulation of cell growth; IEA.
DR InterPro; IPR006208; C; Cytokine knot.
DR InterPro; IPR006207; C; Cytokine knot C.
DR InterPro; IPR000867; I; Inhibitory growth factor.
DR InterPro; IPR000864; TSP1.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF00007; C; Cytokine knot; 1.
DR Pfam; PF00019; IGF1P; 1.
DR Pfam; PF00090; TSP_1; 1.
DR Pfam; PF00093; VWC_1; 1.
DR SMART; SM00041; CT; 1.
DR SMART; SM00041; IB; 1.
DR SMART; SM00209; TSP1; 1.
DR SMART; SM00214; VWC; 1.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00992; TSP1; 1.
DR PROSITE; PS01208; VWF_C_1; 1.
DR PROSITE; PS0184; VWF_C_2; 1.
SQ SEQUENCE 343 AA; 37566 MW; 93F221G5B565A81 CRC64;

Query Match 93.9%; Score 898; DB 2; Length 343;

Best local Similarity 90.7%; Pred. No. 1.4e-75;

Matches 156; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALAAVLEDTFGPDPMTIRANCLVOTTEWSAGSKTGKMGISTRVYNDNASCRLKESRLC 60
DB 172 ALPAFMEETYYGDPSPILIRANCLVOTTEWSAGSKTGKMGISTRVYNDNASCRLKESRLC 231
QY 61 MVRPCADLEENIKKKKICITPTKISKIPKELSGCTSMKTYRAKFCGVCITDGRCTPHR 120
DB 233 MVRPCADLEENIKKKKICITPTKISKIPKELSGCTSMKTYRAKFCGVCITDGRCTPHR 291
QY 121 TATLPVEFKCPDGEVMMKMMFIKTCACHYNCPGNDIFESLYRYKMYGDMA 172
DB 292 TATLPVEFKCPDGEVMMKMMFIKTCACHYNCPGNDIFESLYRYKMYGDMA 343

RESULT 13
ID 0505L5_XENLA PRELIMINARY; PRT; 343 AA.
AC 0505L5;

DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Ctgf protein.
GN Name=Ctgf;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8335;
RX NUCLEOTIDE SEQUENCE.
RP [1]
RC TISSUE=Brain;
RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT Initiative";
RL Dev. Dyn. 225:384-391 (2002).

[2]
RX NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rabe S.S., Louellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., Mewhan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley P.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Kravitz M.T., Skalska U., Small D.E.,
RA Buterfield J.S.N., Kravitz M.T., Skalska U., Small D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maita M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[3]
RX NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RC TISSUE=Brain;
RA Klein S., Gerhard D.S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC094492; AAH94492.1; -; mRNA.
SQ SEQUENCE 343 AA; 37879 MW; 8F448D73C7774FD0 CRC64;

Query Match 93.9%; Score 898; DB 2; Length 343;

Best local Similarity 90.7%; Pred. No. 1.4e-75;

Matches 156; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 ALAAVLEDTFGPDPMTIRANCLVOTTEWSAGSKTGKMGISTRVYNDNASCRLKESRLC 60
DB 172 ALPAFMEETYYGDPSPILIRANCLVOTTEWSAGSKTGKMGISTRVYNDNASCRLKESRLC 231
QY 61 MVRPCADLEENIKKKKICITPTKISKIPKELSGCTSMKTYRAKFCGVCITDGRCTPHR 120
DB 233 MVRPCADLEENIKKKKICITPTKISKIPKELSGCTSMKTYRAKFCGVCITDGRCTPHR 291
QY 121 TATLPVEFKCPDGEVMMKMMFIKTCACHYNCPGNDIFESLYRYKMYGDMA 172
DB 292 TATLPVEFKCPDGEVMMKMMFIKTCACHYNCPGNDIFESLYRYKMYGDMA 343

RESULT 14
ID 05BKU7_XENTR PRELIMINARY; PRT; 343 AA.
AC 05BKU7;
DT 10-MAY-2005 (TREMBLrel. 30, Created)

[illegible]

Oy	121	TTTTTAAATGCTGGAGTTTCACATCCGCGDNDIPESTLYXRKXVGDMA	172
Dd	292	TATTAATGCTGGAGTTTCACATCCGCGDNDIPESTLYXRKXVGDMA	343
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RESULT 15			
O9P80 NOTVI PRELIMINARY; PRT; 347 AA.			
ID	O9P80	NOTVI	PRELIMINARY;
AC	O9P80		
DT	01-MAY-2000	(TREMBLrel. 13, Created)	
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)	
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)	
DE	Connective tissue growth factor.		
GN	Name=ctgf;		
OS	Notocphthalmus viridescens (Eastern newt) (Triturus viridescens).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae;		
OC	Notophthalmus.		
OX	NCBI_TaxID=8316;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Forelimb blastema;		
RX	MEDLINE=99031008; PubMed=9813273; DOI=10.1016/S0378-1119(98)00478-8;		
RA	Cash D.E.; Gates P.B.; Imokawa Y.; Brookes J.P.;		
RT	"Identification of new connective tissue growth factor as a target of		
RL	retinoid regulation in limb blastemal cells."		
RN	Gene 222:119-124(1998).		
RP	[2]		
RC	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Forelimb blastema;		
RA	Gates P.B.;		
RL	Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AJ271167; CAB65965.1; -; mRNA.		
DR	GO; GO:0005576; C:extracellular region; IEA.		
DR	GO; GO:0008083; F:growth factor activity; IEA.		
DR	GO; GO:0005520; F:insulin-like growth factor binding; IEA.		
DR	GO; GO:0001558; P:regulation of cell growth; IEA.		
DR	InterPro; IPR006208; Cys_knot.		
DR	InterPro; IPR006207; Cys_knot_C.		
DR	InterPro; IPR000867; Insl_gro_fac_pr.		
DR	InterPro; IPR000884; TSP1.		
DR	InterPro; IPR001007; WVF_C.		
DR	Pfam; PF00007; Cys_knot; 1.		
DR	Pfam; PF00219; IGFBP; 1.		
DR	Pfam; PF00090; TSP_1; 1.		
DR	Pfam; PF00093; WVC_1.		
DR	SMART; SMART0041; CT; 1.		
DR	SMART; SMART0121; IB; 1.		
DR	SMART; SMART0209; TSP1; 1.		
DR	SMART; SMART0214; WVC; 1.		
DR	PROSITE; PS01185; CTCK_1; 1.		
DR	PROSITE; PS01225; CTCK_2; 1.		
DR	PROSITE; PS00222; IGF_BINDING; 1.		
DR	PROSITE; PS00092; TSP1; 1.		
DR	PROSITE; PS01208; WVC_1; UNKNOWN_1.		
DR	PROSITE; PS01084; WVF_C_2; 1.		
SQ	SEQUENCE 347 AA; 38098 MW; 387E239F27672C1 CRC64;		
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Query Match	93.4%;	Score 893;	DB 2; Length 347;
Best Local Similarity	91.3%;	Prod. No. 4-2e-75;	
Matches 157; Conservative	8;	Mismatches ?;	Indels 0; Gaps 0
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Dd	176	AATAVRGEGTYIGPDSLLRANCLVGTTEMSASCKTGAGISITRVYNDNASCRLEKOSRLC	235
Oy	61	NWRPEADLEENIKKKKKCIPTPKISKPIKTLSGCTSMTYTRAFPGVCTDGRCCTPHR	120
Dd	236	NWRPEADLEENIKKKKKCIPTPKISKPIKTLSGCTSMTYTRAFPGVCTDGRCCTPHR	295
Oy	121	TTTTTAAATGCTGGAGTTTCACATCCGCGDNDIPESTLYXRKXVGDMA	172
Dd	292	TATTAATGCTGGAGTTTCACATCCGCGDNDIPESTLYXRKXVGDMA	343

Mon Jan 9 12:20:10 2006

us-09-461-646-4.rup

Page 11

Search completed: January 9, 2006, 11:19:08
Job time : 162 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2006, 11:13:37 ; Search time 45 Seconds

(without alignments)
316.005 Million cell updates/sec

Title: US-09-461-646-4

Perfect score: 956
Sequence: 1 ALAAVRLDTRGDPPTMIRA.....PGNDIFESLYRRKRYGMA 172Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/1aa/5_COMB.pep:*\n2: /cgn2_6/prodata/1/1aa/6_COMB.pep:*\n3: /cgn2_6/prodata/1/1aa/H_COMB.pep:*\n4: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*\n5: /cgn2_6/prodata/1/1aa/RB_COMB.pep:*\n6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	956	100.0	348	1	US-08-468-847B-14
2	956	100.0	349	1	US-08-167-628-2
3	956	100.0	349	1	US-08-386-680-2
4	956	100.0	349	1	US-08-459-717-2
5	956	100.0	349	1	US-08-712-302-2
6	956	100.0	349	1	US-08-880-031-2
7	956	100.0	349	2	US-09-054-368-2
8	956	100.0	349	2	US-09-097-179-2
9	956	100.0	349	2	US-09-054-274-2
10	956	100.0	349	2	US-09-080-715-2
11	956	100.0	349	2	US-09-056-704-2
12	956	100.0	349	2	US-09-292-036-4
13	956	100.0	349	2	US-09-253-316-26
14	956	100.0	349	2	US-09-142-569-8
15	956	100.0	349	2	US-09-461-688-2
16	956	100.0	349	2	US-09-495-448A-8
17	956	100.0	349	2	US-09-949-016-611
18	956	100.0	349	4	PCT-US96-08140-2
19	934	97.7	348	1	US-09-582-337-2
20	934	97.7	348	1	US-08-468-847B-15
21	934	97.7	348	2	US-09-292-036-3
22	934	97.7	348	2	US-09-142-569-6
23	934	97.7	348	2	US-09-495-448A-6
24	915	95.7	347	2	US-09-187-478-2
25	915	95.7	347	2	US-09-292-036-2
26	560	58.6	98	2	US-09-122-135-6
27	546.5	57.2	351	1	US-08-468-847B-16

28	546.5	57.2	351	2	US-09-495-448A-34	Sequence 34, Appl
29	519	54.3	357	1	US-08-468-847B-17	Sequence 17, Appl
30	519	54.3	357	2	US-09-253-316-25	Sequence 25, Appl
31	487.5	51.0	379	1	US-08-468-847B-11	Sequence 11, Appl
32	487.5	51.0	379	2	US-09-142-569-2	Sequence 2, Appl
33	487.5	51.0	379	2	US-09-495-448A-2	Sequence 2, Appl
34	485.5	50.8	381	2	US-09-142-569-4	Sequence 4, Appl
35	485.5	50.8	381	2	US-09-348-815-2	Sequence 2, Appl
36	485.5	50.8	381	2	US-09-495-448A-4	Sequence 4, Appl
37	479.5	50.2	375	1	US-08-468-847B-13	Sequence 13, Appl
38	479.5	50.2	375	2	US-09-495-448A-33	Sequence 33, Appl
39	469.5	49.1	374	1	US-08-468-847B-12	Sequence 12, Appl
40	468.5	49.0	375	1	US-08-459-101A-2	Sequence 2, Appl
41	423	44.2	345	2	US-09-182-145-11	Sequence 11, Appl
42	423	44.2	367	2	US-09-182-145-12	Sequence 12, Appl
43	405	42.4	339	2	US-09-182-145-32	Sequence 32, Appl
44	405	42.4	372	2	US-09-182-145-33	Sequence 33, Appl
45	404	42.3	339	2	US-09-182-145-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-468-847B-14
; Sequence 14, Application US/08468847B
; Patent No. 5780263
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A. and Adams, Mark D.
; TITLE OF INVENTION: Human CCN-Like Growth Factor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CABELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,847B
; FILING DATE: 6 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MOLLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-468-847B-14

Query Match 100.0%; Score 956; DB 1; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ALAAVRLDTRGDPPTMIRANCLVOTTEWSACSKTCGMSISTRVTNDNASCRLEKQSRIC 60
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Db 177 ALAAVRLDFTFGPDPMTIRANCLVQTTEWSACSKTCGMSGISTRYVTNDNASCRLEKQSRLC 236
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Db 237 MVRPCEADLEBNIKKKKCIPTPKISKPIKELSGCTSMKTYRAKFGVCTDGRCTPHR 296
Qy 121 TTTLTPEFKCPDGEVMMKMMFFIKTCACHYNCPGDNDIFESLYRYKMYGDMA 172
Db 297 TTTLTPEFKCPDGEVMMKMMFFIKTCACHYNCPGDNDIFESLYRYKMYGDMA 348

RESULT 2

US-08-167-628-2
; Sequence 2, Application US/08167628
; Patent No. 5408040
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.,
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,628
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/752,427
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John W.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-1294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-167-628-2

Query Match 100.0%; Score 956; DB 1; Length 349;

Best Local Similarity 100.0%; Pred. No. 1.9e-83; Indels 0; Gaps 0;
Matches 172; Conservative 0; Mismatches 0;

Qy 1 ALAAVRLDFTFGPDPMTIRANCLVQTTEWSACSKTCGMSGISTRYVTNDNASCRLEKQSRLC 60
Db 178 ALAAVRLDFTFGPDPMTIRANCLVQTTEWSACSKTCGMSGISTRYVTNDNASCRLEKQSRLC 237
Qy 61 MVRPCEADLEBNIKKKKCIPTPKISKPIKELSGCTSMKTYRAKFGVCTDGRCTPHR 120
Db 238 MVRPCEADLEBNIKKKKCIPTPKISKPIKELSGCTSMKTYRAKFGVCTDGRCTPHR 297
Qy 121 TTTLTPEFKCPDGEVMMKMMFFIKTCACHYNCPGDNDIFESLYRYKMYGDMA 172
Db 298 TTTLTPEFKCPDGEVMMKMMFFIKTCACHYNCPGDNDIFESLYRYKMYGDMA 349

RESULT 3

US-08-386-680-2

; Sequence 2, Application US/08386680
; Patent No. 5585270
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.,
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,680
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,628
; FILING DATE:
; APPLICATION NUMBER: US/07/752,427
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John W.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-1294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-386-680-2

Query Match 100.0%; Score 956; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e-83; Indels 0; Gaps 0;
Matches 172; Conservative 0; Mismatches 0;

Qy 1 ALAAVRLDFTFGPDPMTIRANCLVQTTEWSACSKTCGMSGISTRYVTNDNASCRLEKQSRLC 60
Db 178 ALAAVRLDFTFGPDPMTIRANCLVQTTEWSACSKTCGMSGISTRYVTNDNASCRLEKQSRLC 237
Qy 61 MVRPCEADLEBNIKKKKCIPTPKISKPIKELSGCTSMKTYRAKFGVCTDGRCTPHR 120
Db 238 MVRPCEADLEBNIKKKKCIPTPKISKPIKELSGCTSMKTYRAKFGVCTDGRCTPHR 297
Qy 121 TTTLTPEFKCPDGEVMMKMMFFIKTCACHYNCPGDNDIFESLYRYKMYGDMA 172
Db 298 TTTLTPEFKCPDGEVMMKMMFFIKTCACHYNCPGDNDIFESLYRYKMYGDMA 349

RESULT 4

US-08-459-717-2
; Sequence 2, Application US/08459717
; Patent No. 5770209
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.,
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla

STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,717
FILING DATE: 02-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/752,427
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-717-2

Query Match 100.0%; Score 956; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AIAAYRLDTFGPDPMTIRANCLVOTTEMSACSKTCGMSISTRVTNDNASCRLEKQSRILC 60
DB 178 AIAAYRLDTFGPDPMTIRANCLVOTTEMSACSKTCGMSISTRVTNDNASCRLEKQSRILC 237

QY 61 WVRPEADLEENIKKGGKCIIRTPKISKPIKELSGCTSMKTYRAKFCGVCCTDGRCTPPH 120
DB 238 WVRPEADLEENIKKGGKCIIRTPKISKPIKELSGCTSMKTYRAKFCGVCCTDGRCTPPH 297

QY 121 TTTLPVEFKCPDGEVWKKMMFIKTCACHYNCPGDNDIFESLYYRKMGDMA 172
DB 298 TTTLPVEFKCPDGEVWKKMMFIKTCACHYNCPGDNDIFESLYYRKMGDMA 349

RESULT 5
US-08-712-302-2
Sequence 2, Application US/08712302
Patent No. 5783187
GENERAL INFORMATION:
APPLICANT: Grotenhorst, Gary R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,302
FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-712-302-2

Query Match 100.0%; Score 956; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AIAAYRLDTFGPDPMTIRANCLVOTTEMSACSKTCGMSISTRVTNDNASCRLEKQSRILC 60
DB 178 AIAAYRLDTFGPDPMTIRANCLVOTTEMSACSKTCGMSISTRVTNDNASCRLEKQSRILC 237

QY 61 WVRPEADLEENIKKGGKCIIRTPKISKPIKELSGCTSMKTYRAKFCGVCCTDGRCTPPH 120
DB 238 WVRPEADLEENIKKGGKCIIRTPKISKPIKELSGCTSMKTYRAKFCGVCCTDGRCTPPH 297

QY 121 TTTLPVEFKCPDGEVWKKMMFIKTCACHYNCPGDNDIFESLYYRKMGDMA 172
DB 298 TTTLPVEFKCPDGEVWKKMMFIKTCACHYNCPGDNDIFESLYYRKMGDMA 349

RESULT 6
US-08-880-031-2
Sequence 2, Application US/08880031
Patent No. 5916756
GENERAL INFORMATION:
APPLICANT: Grotenhorst, Gary R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,031
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110


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; EARLIER APPLICATION NUMBER: 08/386,680
; EARLIER FILING DATE: 1995-02-10
; EARLIER APPLICATION NUMBER: 08/459,717
; EARLIER FILING DATE: 1995-06-02
; EARLIER APPLICATION NUMBER: 08/167,628
; EARLIER FILING DATE: 1993-12-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-054-274-2

Query Match      100.0%; Score 956; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLDTFGPDPMTIRANCLVQTTESASCKTCGMSISTRVTNDNASCRLEKQSRLC 60
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QY 61 MVRPCADLEENIKKGGKCIKRTPKISKPIKFEISGCTSMKTYRAKFCGCTDGRCTPPH 120
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DB 238 MVRPCADLEENIKKGGKCIKRTPKISKPIKFEISGCTSMKTYRAKFCGCTDGRCTPPH 297
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DB 298 TTTLPVFEKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYRRMYGDMA 349
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RESULT 10
US-09-080-715-2
; Sequence 2, Application US/09080715
; Patent No. 6130864
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,715
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,628
; FILING DATE:
; APPLICATION NUMBER: US/07/752,427
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weherell, Jr., Ph.D., John W.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-1294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-09-080-715-2

Query Match      100.0%; Score 956; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLDTFGPDPMTIRANCLVQTTESASCKTCGMSISTRVTNDNASCRLEKQSRLC 60
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DB 178 ALAAVRLDTFGPDPMTIRANCLVQTTESASCKTCGMSISTRVTNDNASCRLEKQSRLC 237
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QY 61 MVRPCADLEENIKKGGKCIKRTPKISKPIKFEISGCTSMKTYRAKFCGCTDGRCTPPH 120
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QY 121 TTTLPVFEKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYRRMYGDMA 172
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DB 298 TTTLPVFEKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYRRMYGDMA 349
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RESULT 11
US-09-056-704-2
; Sequence 2, Application US/09056704
; Patent No. 6232064
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham, Jr., Douglas M.
; TITLE OF INVENTION: METHODS OF DIAGNOSING A PATHOLOGY
; TITLE OF INVENTION: CHARACTERIZED BY A CELL PROLIFERATIVE
; TITLE OF INVENTION: DISORDER ASSOCIATED WITH CONNECTIVE
; TITLE OF INVENTION: TISSUE GROWTH FACTOR (amended)
; FILE REFERENCE: 0744/003002
; CURRENT APPLICATION NUMBER: US/09/056,704
; CURRENT FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: 08/386,680
; EARLIER FILING DATE: 1995-02-10
; EARLIER APPLICATION NUMBER: 08/459,717
; EARLIER FILING DATE: 1995-06-02
; EARLIER APPLICATION NUMBER: 08/167,628
; EARLIER FILING DATE: 1993-12-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-056-704-2

Query Match      100.0%; Score 956; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 MVRPCADLEENIKKGGKCIKRTPKISKPIKFEISGCTSMKTYRAKFCGCTDGRCTPPH 120
    |||
DB 238 MVRPCADLEENIKKGGKCIKRTPKISKPIKFEISGCTSMKTYRAKFCGCTDGRCTPPH 297
    |||

QY 121 TTTLPVFEKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYRRMYGDMA 172
    |||
DB 298 TTTLPVFEKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYRRMYGDMA 349
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RESULT 12
US-09-292-036-4
; Sequence 4, Application US/09292036
; Patent No. 6358741
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
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/ CURRENT FILING DATE: 1999-12-14
 / PRIOR APPLICATION NUMBER: 60/112,240
 / PRIOR FILING DATE: 1998-12-14
 / PRIOR APPLICATION NUMBER: 60/112,241
 / PRIOR FILING DATE: 1998-12-14
 / NUMBER OF SEQ ID NOS: 4
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO: 2
 / LENGTH: 349
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-09-461-688-2

Query Match 100.0%; Score 956; DB 2; Length 349;
 Best Local Similarity 100.0%; Pred. No. 1.9e-83;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	178	ALAAVRLIEDTPGPDPTMIRANCLVOTTEWSACSKTCGMGISRTVTNDNASCRLKOSRLC	237
Qy	61	MYRPEADLEENIKKGKCIKRTPKISKPIKFEISGCTSMKTYRAKFCGVCTDGRCTPHR	120
Db	238	MYRPEADLEENIKKGKCIKRTPKISKPIKFEISGCTSMKTYRAKFCGVCTDGRCTPHR	297
Qy	121	TTTTLPEVEFKCPDGEVWKKMMFIKTCACHYNCPGDNDIFESLYYRRMYGDMA	172
Db	298	TTTTLPEVEFKCPDGEVWKKMMFIKTCACHYNCPGDNDIFESLYYRRMYGDMA	349

Search completed: January 9, 2006, 11:20:54
 Job time : 46 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2006, 11:19:18 ; Search time 115 Seconds
(without alignments)
624.927 Million cell updates/sec

Title: US-09-461-646-4

Perfect score: 956
Sequence: 1 ALAAVRLDPTGPDPTMIRA.....PQNDIFSLYRKRYGDM 172

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	956	100.0	172	4 US-10-658-856-4	Sequence 4, Appl
2	956	100.0	348	3 US-09-853-625B-14	Sequence 14, Appl
3	956	100.0	349	4 US-10-101-040-4	Sequence 4, Appl
4	956	100.0	349	4 US-10-011-859-26	Sequence 26, Appl
5	956	100.0	349	4 US-10-053-753-8	Sequence 8, Appl
6	956	100.0	349	4 US-10-060-036-173	Sequence 173, Appl
7	956	100.0	349	4 US-10-171-311-46	Sequence 46, Appl
8	956	100.0	349	4 US-10-205-823-78	Sequence 78, Appl
9	956	100.0	349	4 US-10-245-977-2	Sequence 2, Appl
10	956	100.0	349	4 US-10-315-568-2	Sequence 2, Appl
11	956	100.0	349	4 US-10-394-015-4	Sequence 4, Appl
12	956	100.0	349	4 US-10-131-985-7	Sequence 7, Appl
13	956	100.0	349	4 US-10-182-432-8	Sequence 8, Appl
14	956	100.0	349	4 US-10-338-587A-2	Sequence 2, Appl
15	956	100.0	349	4 US-10-428-487-4	Sequence 4, Appl
16	956	100.0	349	4 US-10-464-368-55	Sequence 55, Appl
17	956	100.0	349	4 US-10-658-856-2	Sequence 2, Appl
18	956	100.0	349	4 US-10-627-604-14	Sequence 14, Appl
19	956	100.0	349	4 US-10-721-336-3	Sequence 3, Appl
20	956	100.0	349	4 US-10-755-889-60	Sequence 60, Appl
21	956	100.0	349	5 US-10-858-186-2	Sequence 2, Appl
22	956	100.0	349	5 US-10-902-895-8	Sequence 8, Appl
23	956	100.0	349	5 US-10-901-417-7	Sequence 7, Appl
24	956	100.0	349	5 US-10-627-604-14	Sequence 14, Appl
25	956	100.0	349	5 US-10-955-860A-1	Sequence 1, Appl
26	956	100.0	349	6 US-11-051-654-78	Sequence 78, Appl
27	956	100.0	349	6 US-11-149-564-26	Sequence 26, Appl

28	938	98.1	226	5 US-10-617-316-132	Sequence 132, Appl
29	938	98.1	226	5 US-10-617-316-163	Sequence 163, Appl
30	938	98.1	349	4 US-10-245-977-5	Sequence 5, Appl
31	937	98.0	349	4 US-10-245-977-6	Sequence 6, Appl
32	934	97.7	347	4 US-10-245-977-7	Sequence 7, Appl
33	934	97.7	347	4 US-10-390-986-2	Sequence 2, Appl
34	934	97.7	347	4 US-10-464-368-56	Sequence 56, Appl
35	934	97.7	348	3 US-09-853-625B-15	Sequence 15, Appl
36	934	97.7	348	4 US-10-101-040-3	Sequence 3, Appl
37	934	97.7	348	4 US-10-053-753-6	Sequence 6, Appl
38	934	97.7	348	4 US-10-245-977-8	Sequence 8, Appl
39	934	97.7	348	4 US-10-182-432-6	Sequence 6, Appl
40	934	97.7	348	4 US-10-464-368-54	Sequence 54, Appl
41	934	97.7	348	4 US-10-627-604-15	Sequence 15, Appl
42	934	97.7	348	5 US-10-902-895-6	Sequence 6, Appl
43	934	97.7	348	5 US-10-627-604-15	Sequence 15, Appl
44	915	95.7	347	4 US-10-080-173-2	Sequence 2, Appl
45	915	95.7	347	4 US-10-101-040-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-10-658-856-4
; Sequence 4, Application US/10658856
; Publication No. US20040092450A1
; GENERAL INFORMATION:
; APPLICANT: Fibrogen, Inc.
; APPLICANT: Fibrogen, Gary
; APPLICANT: Neff, Thomas
; TITLE OF INVENTION: Connective Tissue Growth Factor Fragments and Methods and Uses Th
; FILE REFERENCE: FIBRO130-2 US/10/658,856
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US/09/461,646
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: 60/112,240
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/112,241
; PRIOR FILING DATE: 1998-12-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-856-4
Query Match          100.0%; Score 956; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 8,4e-84;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ALAAVRLDPTGPDPTMIRANCLVOTTEWSACSKTCGMGISTFVTNDNASCRLEKOSRLC 60
1 ALAAVRLDPTGPDPTMIRANCLVOTTEWSACSKTCGMGISTFVTNDNASCRLEKOSRLC 60
61 MYRPGCADLEBNIKKGGKICIRTPKISKPIKIFELSGTSMKTYRAKCGVCTDGRCTPPH 120
61 MYRPGCADLEBNIKKGGKICIRTPKISKPIKIFELSGTSMKTYRAKCGVCTDGRCTPPH 120
121 TTTLPEVFKCPDGEVKKMMFMFKTCACHYNCGDDNDFESLYRKMYGDM 172
121 TTTLPEVFKCPDGEVKKMMFMFKTCACHYNCGDDNDFESLYRKMYGDM 172
RESULT 2
US-09-853-625B-14
; Sequence 14, Application US/09853625B
; Patent No. US2002004304A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A. and Adams, Mark D.
; TITLE OF INVENTION: Human CCN-Like Growth Factor
```

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/853,6258
FILING DATE: 14-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/053,587
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-442
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 348 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: <Unknown>
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-853-6258-14

Query Match 100.0%; Score 956; DB 3; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLDFTGPDPTMIRANCLVQTTEWSACSKTCGWSGISTRVTNDNASCRLEKQSRLC 60
DB 177 ALAAVRLDFTGPDPTMIRANCLVQTTEWSACSKTCGWSGISTRVTNDNASCRLEKQSRLC 236

QY 61 MVRPCEADLEENIKKKKCIPTPKISKPIKELSGCTSMKTYRAKFCGVCCTDGRCTPHR 120
DB 237 MVRPCEADLEENIKKKKCIPTPKISKPIKELSGCTSMKTYRAKFCGVCCTDGRCTPHR 296

QY 121 TTTLPEFKCPDGEVMMKMMFIKTCACHNCPGDNDIFESLYYRKMYGDMA 172
DB 297 TTTLPEFKCPDGEVMMKMMFIKTCACHNCPGDNDIFESLYYRKMYGDMA 348

RESULT 3
US-10-101-040-4
Sequence 4, Application US/10101040
Publication No. US20020142353A1
GENERAL INFORMATION:
APPLICANT: FIBROGEN, INC
APPLICANT: SCHMIDT, Brian
APPLICANT: ALLEN, Margaret
APPLICANT: SVERDRUP, Fran
APPLICANT: CARMICHAEL, David
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF
FILE REFERENCE: FIBRO1100-1
CURRENT APPLICATION NUMBER: US/10/101,040
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/292,036
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 09/292,036

PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 09/187,478
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 349
TYPE: PRT
ORGANISM: Human
US-10-101-040-4

Query Match 100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLDFTGPDPTMIRANCLVQTTEWSACSKTCGWSGISTRVTNDNASCRLEKQSRLC 60
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QY 121 TTTLPEFKCPDGEVMMKMMFIKTCACHNCPGDNDIFESLYYRKMYGDMA 172
DB 298 TTTLPEFKCPDGEVMMKMMFIKTCACHNCPGDNDIFESLYYRKMYGDMA 349

RESULT 4
US-10-011-859-26
Sequence 26, Application US/10011859
Publication No. US20020147328A1
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Jaegers, Stephen R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR HOMOLOGS
FILE REFERENCE: 97-75
CURRENT APPLICATION NUMBER: US/10/011,859
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/253,116
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-19
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/075,300
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-10-011-859-26

Query Match 100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLDFTGPDPTMIRANCLVQTTEWSACSKTCGWSGISTRVTNDNASCRLEKQSRLC 60
DB 178 ALAAVRLDFTGPDPTMIRANCLVQTTEWSACSKTCGWSGISTRVTNDNASCRLEKQSRLC 237

QY 61 MVRPCEADLEENIKKKKCIPTPKISKPIKELSGCTSMKTYRAKFCGVCCTDGRCTPHR 120
DB 238 MVRPCEADLEENIKKKKCIPTPKISKPIKELSGCTSMKTYRAKFCGVCCTDGRCTPHR 297

QY 121 TTTLPEFKCPDGEVMMKMMFIKTCACHNCPGDNDIFESLYYRKMYGDMA 172
DB 298 TTTLPEFKCPDGEVMMKMMFIKTCACHNCPGDNDIFESLYYRKMYGDMA 349

RESULT 5
US-10-053-753-8
Sequence 8, Application US/10053753
Publication No. US20020150986A1
GENERAL INFORMATION:

APPLICANT: Lau, Lester F.
TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,753
FILING DATE: 22-Jan-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28758/33766
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "CTG amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-053-753-8
Query Match 100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1,8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAAVRLDPTFGDPPTMIRANCLVOTTEWSASCKTGMSISTRVTNDNASCRLEKQSRIC 60
DB 178 ALAAVRLDPTFGDPPTMIRANCLVOTTEWSASCKTGMSISTRVTNDNASCRLEKQSRIC 237
QY 61 MYRPEADLEENIKKGGKCIPTPKISKPIKPELSGCTSMKTYRAKCGVCTDGRCTPPH 120
DB 238 MYRPEADLEENIKKGGKCIPTPKISKPIKPELSGCTSMKTYRAKCGVCTDGRCTPPH 297
QY 121 TTTLPEFKCPDGEVWKKMMFIKTCACHYNGDNDIFESLYYRMYGDM 172
DB 298 TTTLPEFKCPDGEVWKKMMFIKTCACHYNGDNDIFESLYYRMYGDM 349
RESULT 6
US-10-060-036-173
Sequence 173, Application US/10060036
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Perlberg, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yugu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121, 566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30

NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 173
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-10-060-036-173
Query Match 100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1,8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAAVRLDPTFGDPPTMIRANCLVOTTEWSASCKTGMSISTRVTNDNASCRLEKQSRIC 60
DB 178 ALAAVRLDPTFGDPPTMIRANCLVOTTEWSASCKTGMSISTRVTNDNASCRLEKQSRIC 237
QY 61 MYRPEADLEENIKKGGKCIPTPKISKPIKPELSGCTSMKTYRAKCGVCTDGRCTPPH 120
DB 238 MYRPEADLEENIKKGGKCIPTPKISKPIKPELSGCTSMKTYRAKCGVCTDGRCTPPH 297
QY 121 TTTLPEFKCPDGEVWKKMMFIKTCACHYNGDNDIFESLYYRMYGDM 172
DB 298 TTTLPEFKCPDGEVWKKMMFIKTCACHYNGDNDIFESLYYRMYGDM 349
RESULT 7
US-10-171-311-46
Sequence 46, Application US/10171311
Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Glatt, Karen
APPLICANT: Ganavarapu, Manjula
APPLICANT: Hoersch, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 46
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-10-171-311-46
Query Match 100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1,8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALAAVRLDPTFGDPPTMIRANCLVOTTEWSASCKTGMSISTRVTNDNASCRLEKQSRIC 60
DB 178 ALAAVRLDPTFGDPPTMIRANCLVOTTEWSASCKTGMSISTRVTNDNASCRLEKQSRIC 237
QY 61 MYRPEADLEENIKKGGKCIPTPKISKPIKPELSGCTSMKTYRAKCGVCTDGRCTPPH 120
DB 238 MYRPEADLEENIKKGGKCIPTPKISKPIKPELSGCTSMKTYRAKCGVCTDGRCTPPH 297
QY 121 TTTLPEFKCPDGEVWKKMMFIKTCACHYNGDNDIFESLYYRMYGDM 172
DB 298 TTTLPEFKCPDGEVWKKMMFIKTCACHYNGDNDIFESLYYRMYGDM 349

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RESULT 8
US-10-205-823-78
; Sequence 78, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatc, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205, 823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-78

Query Match          100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAYRLDPTFGPDPPTMIRANCLVQTTWMSACSKTCGMGISTRTVNDNASCRLEKOSRLC 60
DB 178 ALAAYRLDPTFGPDPPTMIRANCLVQTTWMSACSKTCGMGISTRTVNDNASCRLEKOSRLC 237
QY 61 MVRPCEADLEENIKKGGKCIKRTPKISKPIKPELSGCTSMKTYRAKFCGVCCTDGRCTPHR 120
DB 238 MVRPCEADLEENIKKGGKCIKRTPKISKPIKPELSGCTSMKTYRAKFCGVCCTDGRCTPHR 297
QY 121 TTTLPEVEFKCPDGEVKKMMMFITKCAHYNCPGNDIFESLYYRKMYGDMA 172
DB 298 TTTLPEVEFKCPDGEVKKMMMFITKCAHYNCPGNDIFESLYYRKMYGDMA 349

RESULT 9
US-10-245-977-2
; Sequence 2, Application US/10245977
; Publication No. US20030113816A1
; GENERAL INFORMATION:
; APPLICANT: Weitzer, Stephen L.
; APPLICANT: Ueinger, William R.
; TITLE OF INVENTION: METHODS OF ASSAYING CONNECTIVE TISSUE GROWTH FACTOR
; FILE REFERENCE: FP0812 US
; CURRENT APPLICATION NUMBER: US/10/245,977
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/323,305
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 8
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-977-2

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Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 178 ALAAYRLDPTFGPDPPTMIRANCLVQTTWMSACSKTCGMGISTRTVNDNASCRLEKOSRLC 237
QY 61 MVRPCEADLEENIKKGGKCIKRTPKISKPIKPELSGCTSMKTYRAKFCGVCCTDGRCTPHR 120
DB 238 MVRPCEADLEENIKKGGKCIKRTPKISKPIKPELSGCTSMKTYRAKFCGVCCTDGRCTPHR 297
QY 121 TTTLPEVEFKCPDGEVKKMMMFITKCAHYNCPGNDIFESLYYRKMYGDMA 172
DB 298 TTTLPEVEFKCPDGEVKKMMMFITKCAHYNCPGNDIFESLYYRKMYGDMA 349

RESULT 10
US-10-315-568-2
; Sequence 2, Application US/10315568
; Publication No. US20030180300A1
; GENERAL INFORMATION:
; APPLICANT: Fibrogen, Inc.
; APPLICANT: Grotendorst, Gary R.
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR FRAGMENTS AND METHODS TH
; FILE REFERENCE: FIBRO1140-3
; CURRENT APPLICATION NUMBER: US/10/315,568
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 09/461,688
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: US 60/112,240
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: US 60/112,241
; PRIOR FILING DATE: 1998-12-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-315-568-2

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Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 178 ALAAYRLDPTFGPDPPTMIRANCLVQTTWMSACSKTCGMGISTRTVNDNASCRLEKOSRLC 237
QY 61 MVRPCEADLEENIKKGGKCIKRTPKISKPIKPELSGCTSMKTYRAKFCGVCCTDGRCTPHR 120
DB 238 MVRPCEADLEENIKKGGKCIKRTPKISKPIKPELSGCTSMKTYRAKFCGVCCTDGRCTPHR 297
QY 121 TTTLPEVEFKCPDGEVKKMMMFITKCAHYNCPGNDIFESLYYRKMYGDMA 172
DB 298 TTTLPEVEFKCPDGEVKKMMMFITKCAHYNCPGNDIFESLYYRKMYGDMA 349

RESULT 11
US-10-394-015-4
; Sequence 4, Application US/10394015
; Publication No. US20030180891A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Ruben, Steven M.
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; TITLE OF INVENTION: Connective Tissue Growth Factor-4
; FILE REFERENCE: Pf467
; CURRENT APPLICATION NUMBER: US/10/394,015
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US/09/325,019
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/088,320
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-394-015-4

Query Match          100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 178 ALAAVRLDTFGDDPTMIRANCLVOTTEWSASCTGCMGISTRVTNNDNASCRLEKOSRLC 237
    |||

QY 61 MYRPCADLEENIKKGKCCIRTPKISKPIKFEISGCTSMKTYRAKFCGCTDGRCTPPHR 120
    |||
DB 238 MYRPCADLEENIKKGKCCIRTPKISKPIKFEISGCTSMKTYRAKFCGCTDGRCTPPHR 297
    |||

QY 121 TTTLPEVFKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYYRKMYGDMA 172
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DB 298 TTTLPEVFKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYYRKMYGDMA 349
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RESULT 12
; US-10-131-985-7
; Sequence 7, Application US/10131985
; Publication No. US20030199440A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768, 8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-131-985-7

Query Match          100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALAAVRLDTFGDDPTMIRANCLVOTTEWSASCTGCMGISTRVTNNDNASCRLEKOSRLC 60
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DB 178 ALAAVRLDTFGDDPTMIRANCLVOTTEWSASCTGCMGISTRVTNNDNASCRLEKOSRLC 237
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QY 61 MYRPCADLEENIKKGKCCIRTPKISKPIKFEISGCTSMKTYRAKFCGCTDGRCTPPHR 120
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DB 238 MYRPCADLEENIKKGKCCIRTPKISKPIKFEISGCTSMKTYRAKFCGCTDGRCTPPHR 297
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QY 121 TTTLPEVFKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYYRKMYGDMA 172
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DB 298 TTTLPEVFKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYYRKMYGDMA 349
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Query Match          100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 TTTLPEVFKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYYRKMYGDMA 172
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DB 298 TTTLPEVFKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYYRKMYGDMA 349
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DB 298 TTTLPEVFKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYYRKMYGDMA 349
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RESULT 13
; US-10-182-432-8
; Sequence 8, Application US/10182432
; Publication No. US20040002124A1
; GENERAL INFORMATION:
; APPLICANT: LAU, Lester F., YEUNG, Cho-Yau, and GREENSPAN, Jeffrey A.
; TITLE OF INVENTION: CYR61 COMPOSITIONS AND METHODS
; FILE REFERENCE: 214448/00029
; CURRENT APPLICATION NUMBER: US/10/182,432
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-182-432-8

Query Match          100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 178 ALAAVRLDTFGDDPTMIRANCLVOTTEWSASCTGCMGISTRVTNNDNASCRLEKOSRLC 237
    |||

QY 61 MYRPCADLEENIKKGKCCIRTPKISKPIKFEISGCTSMKTYRAKFCGCTDGRCTPPHR 120
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DB 238 MYRPCADLEENIKKGKCCIRTPKISKPIKFEISGCTSMKTYRAKFCGCTDGRCTPPHR 297
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QY 121 TTTLPEVFKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYYRKMYGDMA 172
    |||
DB 298 TTTLPEVFKCPDGEVWKKMMFIKTCACHYNCPGNDIFESLYYRKMYGDMA 349
    |||

RESULT 14
; US-10-338-587A-2
; Sequence 2, Application US/10338587A
; Publication No. US20040005319A1
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF SOUTH FLORIDA
; APPLICANT: GROTEENDORST, Gary R.
; APPLICANT: BRADHAM, Douglas M.
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; FILE REFERENCE: USF1100-15
; CURRENT APPLICATION NUMBER: US/10/338,587A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 09/054,363
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: US 08/459,717
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: US 08/386,680
; PRIOR FILING DATE: 1995-02-10
; PRIOR APPLICATION NUMBER: US 08/167,628
; PRIOR FILING DATE: 1993-12-14
; PRIOR APPLICATION NUMBER: US 07/752,427
; PRIOR FILING DATE: 1991-08-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-338-587A-2

Query Match          100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 178 ALAAVRLDPTFGPPTMIRANCLVQTTWMSACSKTCGMSISTRVTNDNASCRLEKOSRLC 237
    |||
QY 61 MVRPEADLEENIKKKKCIPTPKISKPIKELSGCTSMKTYRAKFCGVCTDGRCTPHR 120
    |||
DB 238 MVRPEADLEENIKKKKCIPTPKISKPIKELSGCTSMKTYRAKFCGVCTDGRCTPHR 297
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QY 121 TTTLPEVFKCPDGEVMMKMMFIKTCACHYNCPGNDIFESLYYRKMYGDMA 172
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DB 298 TTTLPEVFKCPDGEVMMKMMFIKTCACHYNCPGNDIFESLYYRKMYGDMA 349
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RESULT 15
US-10-428-487-44

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; Sequence 44, Application US/10428487
; Publication No. US20040006780A1
; GENERAL INFORMATION:
; APPLICANT: GERBER, HANS-PETER
; TITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING THEM
; FILE REFERENCE: 09800080-0103
; CURRENT APPLICATION NUMBER: US/10/428,487
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/815,153
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,201
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 44
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-428-487-44
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Query Match 100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 178 ALAAVRLDPTFGPPTMIRANCLVQTTWMSACSKTCGMSISTRVTNDNASCRLEKOSRLC 237
    |||
QY 61 MVRPEADLEENIKKKKCIPTPKISKPIKELSGCTSMKTYRAKFCGVCTDGRCTPHR 120
    |||
DB 238 MVRPEADLEENIKKKKCIPTPKISKPIKELSGCTSMKTYRAKFCGVCTDGRCTPHR 297
    |||
QY 121 TTTLPEVFKCPDGEVMMKMMFIKTCACHYNCPGNDIFESLYYRKMYGDMA 172
    |||
DB 298 TTTLPEVFKCPDGEVMMKMMFIKTCACHYNCPGNDIFESLYYRKMYGDMA 349
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Search completed: January 9, 2006, 11:30:43
Job time : 116 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM protein - protein search, using sw model

Run on: January 9, 2006, 11:20:03 ; Search time 27 Seconds

(without alignments)
54.108 Million cell updates/sec

Title: US-09-461-646-4

Perfect score: 1 ALAAVRLBETFGPPDPTMIRA.....RGDNDIFESLYRRKMGDMA 172

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 61141 seqs, 8493638 residues

Total number of hits satisfying chosen parameters: 61141

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_New.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	956	100.0	349	7	US-11-067-121-14
2	956	100.0	397	6	US-10-821-234-1020
3	934	97.7	348	7	US-11-067-121-5
4	925	96.8	317	7	US-11-094-519A-38
5	848	88.7	322	7	US-11-067-121-15
6	432	45.2	74	7	US-11-094-519A-46
7	148	15.5	250	6	US-10-131-826A-320
8	103.5	10.8	1216	7	US-11-039-398-12
9	103.5	10.8	1222	7	US-11-039-398-8
10	103.5	10.8	1235	7	US-11-039-398-16
11	103.5	10.8	1252	7	US-11-039-398-20
12	102	10.7	1213	7	US-11-039-398-14
13	102	10.7	1232	7	US-11-039-398-10
14	102	10.7	1232	7	US-11-039-398-18
15	102	10.7	1249	7	US-11-039-398-22
16	94.5	9.9	1210	6	US-10-624-932-26
17	94.5	9.9	1454	7	US-11-109-157A-2
18	94.5	9.9	1686	7	US-11-109-157A-11
19	89	9.3	938	7	US-11-109-157A-18
20	89	9.3	1221	7	US-11-109-157A-17
21	87.5	9.2	386	7	US-11-143-986-2
22	87.5	9.2	386	7	US-11-143-986-3
23	87	9.1	1170	6	US-10-831-997-2
24	87	9.1	1170	6	US-10-995-561-594
25	87	9.1	1170	6	US-10-995-561-595

26	87	9.1	1170	6	US-10-995-561-596	Sequence 596, App
27	87	9.1	1170	7	US-11-046-456-28	Sequence 28, Appl
28	87	9.1	1170	7	US-11-046-644-28	Sequence 28, Appl
29	86.5	9.0	69	7	US-11-022-562-224	Sequence 224, App
30	86.5	9.0	1211	7	US-11-166-284-4	Sequence 4, Appl
31	84.5	8.8	372	7	US-11-143-986-5	Sequence 5, Appl
32	84.5	8.8	372	7	US-11-143-986-6	Sequence 6, Appl
33	84.5	8.8	397	7	US-11-022-562-223	Sequence 223, App
34	82	8.6	1907	7	US-11-039-398-25	Sequence 25, Appl
35	81.5	8.5	2515	7	US-11-113-424-53	Sequence 53, Appl
36	81.5	8.5	4655	6	US-10-995-561-556	Sequence 556, App
37	81	8.5	795	7	US-11-109-157A-14	Sequence 14, Appl
38	81	8.5	1072	7	US-11-109-157A-13	Sequence 13, Appl
39	81	8.5	1172	7	US-11-186-284-203	Sequence 203, App
40	79.5	8.3	5179	7	US-11-108-172-1068	Sequence 1068, App
41	79	8.3	2764	6	US-10-995-561-691	Sequence 691, App
42	79	8.3	2813	6	US-10-995-561-688	Sequence 688, App
43	79	8.3	2919	6	US-10-821-234-1133	Sequence 1133, App
44	76.5	8.0	335	7	US-11-136-619-30	Sequence 30, Appl
45	76.5	8.0	351	7	US-11-136-619-14	Sequence 14, Appl

ALIGNMENTS

```
RESULT 1
US-11-067-121-14
; Sequence 14, Application US/11067121
; Publication No. US20050261185A1
; GENERAL INFORMATION:
; APPLICANT: Martijn, Cecile
; APPLICANT: Rondahl, Lena
; TITLE OF INVENTION: THERAPEUTIC PROTEINS
; FILE REFERENCE: 18909-002001
; CURRENT FILING DATE: US/11/067,121
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/576,445
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: SE 0400489-1
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-121-14

Query Match      100.0%; Score 956; DB 7; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.3e-88;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ALAAVRLBETFGPPDPTMIRANCLVOTTEWSASCKTGKMGISTRTVNDNASCRLEKQSRIC 60
DB      178 ALAAVRLBETFGPPDPTMIRANCLVOTTEWSASCKTGKMGISTRTVNDNASCRLEKQSRIC 237
QY      61 MYRPEADLEENIKKGGKCCIRTPKISKPIKFEISGCTSMKTYRAKCGCTDGRCTPPR 120
DB      238 MYRPEADLEENIKKGGKCCIRTPKISKPIKFEISGCTSMKTYRAKCGCTDGRCTPPR 297
QY      121 TTTLPVRFKCPGGEVWKKMMKPKTCACGYNCGDNDIFESLYRRKMGDMA 172
DB      298 TTTLPVRFKCPGGEVWKKMMKPKTCACGYNCGDNDIFESLYRRKMGDMA 349

RESULT 2
US-10-821-234-1020
; Sequence 1020, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgitte
; APPLICANT: Andarmant, Susan
```

```

: APPLICANT Tang, Y. Tom
: TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
: FILE REFERENCE: 821A
: CURRENT APPLICATION NUMBER: US/10/821,234
: CURRENT FILING DATE: 2004-04-07
: PRIOR APPLICATION NUMBER: US 60/462,047
: PRIOR FILING DATE: 2003-04-07
: NUMBER OF SEQ ID NOS: 1704
: SOFTWARE: pt_seq_genes Version 1.0
: SEQ ID NO 1020
: LENGTH: 397
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-821-234-1020

```

Query March	100.0%	Score 956;	DB 6;	Length 397;
Best Local Similarity	100.0%	Pred. NC 1.5e-86;		
Matches 172;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	226	61	286	121	346
QY	ALAAVLEDPFGDPMIRANCLVOTTEMSASCKTCGIGISTRVYTNNAASCRLEKOSRLC	ALAAVRIEDTFGDPMIRANCLVOTTEMSASCKTCGIGISTRVYTNNAASCRLEKOSRLC	MVRPCEADLEENIKKKKCCIRTPKTSKIPKEFLSGCTSMKYRAKFGVCTDGCCTPHR	MVRPCEADLEENIKKKKCCIRTPKTSKIPKEFLSGCTSMKYRAKFGVCTDGCCTPHR	TTTTLPVPEFKCPDGEVYMKKKMMFVYKTCACHYNGPGNDIFESLYYRKMYGDMA	TTTTLPVPEFKCPDGEVYMKKKMMFVYKTCACHYNGPGNDIFESLYYRKMYGDMA
	60	285	120	345	172	397

RESULT 3

US-11-067-121-5
; Sequence 5, Application US/11067121
; Publication No. US20050261185A1

```

1  APPLICANT: Martijn, Cecile
2  APPLICANT: Rondahl, Lena
3  TITLE OF INVENTION: THERAPEUTIC PROTEINS
4  FILE REFERENCE: 18909-002001
5  CURRENT APPLICATION NUMBER: US/11/067,121
6  CURRENT FILING DATE: 2005-02-25
7  PRIOR APPLICATION NUMBER: US 60/576,445
8  PRIOR FILING DATE: 2004-06-02
9  PRIOR APPLICATION NUMBER: SE 0400489-1
10 PRIOR FILING DATE: 2004-02-27
11 NUMBER OF SEQ ID NOS: 20
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 5
14 LENGTH: 348
15 TYPE: PRT
16 ORGANISM: Mus musculus
17 US-11-067-121-5

```

Query Match	97.7%	Score 934	DB 7	Length 348
Best Local Similarity	95.9%	Pred. No. 2e-86		
Matches 165	Conservative 5	Mismatches 2	Indels 0	Gaps 0

Qy	1	ALAAVRIEDFDGDPIMIRANCLIVÖTTESASASTKCGMGISIRRYVNDNDSARLEKÖSRLC	60
Db	177	ALAAVRIEDFDGDPIMIRANCLIVÖTTESASASTKCGMGISIRRYVNDNTPCRLEKÖSRLC	236
Qy	61	MVRPCEDAEENIKKKKKCIRPKISKIPKELSCTGCTSMKTYRAKFGCVGCDGDCCPHR	120
Db	237	MVRPCEDAEENIKKKKKCIRPKIAKAPVKEFELSCTGCTSVKTYRAKFGCVGCDGDCCTPHR	296
Qy	121	TTTTLPVBFCKPDGEMKKMMMFIKTCACAYNCPGNDIFESLYRXRWGMDAA	172
Db	297	TTTTLPVBFCKPDGEMKKMMFIKTCACAYNCPGNDIFESLYRXRWGMDAA	348

RESULT 4

US-11-094-519A-38
 ; Sequence 38, Application US/11094519A
 ; Publication No. US20050281810A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BERNSTEIN, Jeanne
 ; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
 ; FILE REFERENCE: 2786-0140P
 ; CURRENT APPLICATION NUMBER: US/11/094,519A
 ; CURRENT FILING DATE: 2005-03-31
 ; PRIOR APPLICATION NUMBER: US/09/695,293
 ; PRIOR FILING DATE: 2000-10-25
 ; PRIOR APPLICATION NUMBER: IL 123558
 ; PRIOR FILING DATE: 1999-10-25
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 38
 ; LENGTH: 317
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-094-519A-38

Query Match	96.8%;	Score 925;	DB 7;	Length 317;
Best Local Similarity	-99.4%;	Pred. No. 1.4e-85;		
Matches 165;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

QY	7	LEDFTGPDPTMI	RAACLVQVOTTEWMSACS	KTCGGIGISTRV	YNDNAS	CRLERQSR	LCMVR	PCB	66
Db	152	LEDFTGPDPTMI <td>RAACLVQVOTTEWMSACS <td>KTCGGIGISTRV <td>YNDNAS <td>CRLERQSR <td>LCMVR <td>PCB</td> <td>211</td> </td></td></td></td></td>	RAACLVQVOTTEWMSACS <td>KTCGGIGISTRV <td>YNDNAS <td>CRLERQSR <td>LCMVR <td>PCB</td> <td>211</td> </td></td></td></td>	KTCGGIGISTRV <td>YNDNAS <td>CRLERQSR <td>LCMVR <td>PCB</td> <td>211</td> </td></td></td>	YNDNAS <td>CRLERQSR <td>LCMVR <td>PCB</td> <td>211</td> </td></td>	CRLERQSR <td>LCMVR <td>PCB</td> <td>211</td> </td>	LCMVR <td>PCB</td> <td>211</td>	PCB	211
QY	67	ADLEENIKKKKKC	IRTPKISPR	IKFELS	SGCTSM	KYRAKFC	GVCDTGR	CCTPHRTTTL	EV
Db	212	SDLEENIKKKKKC	IRTPKISPR	IKFELS	SGCTSM	KYRAKFC	GVCDTGR	CCTPHRTTTL	EV
QY	127	EFKCGDEGVMKKNNMF	IKTCCACHY	CCPGNDNIFES	LYRKMY	GDNA			172
Db	272	EFKCGDEGVMKKNNMF	IKTCCACHY	CCPGNDNIFES	LYRKMY	GDNA			317

RESULT 5

```

US-11-067-121-15
; Sequence 15, Application US/11067721
; Publication NO. US20050261185A1
;
; GENERAL INFORMATION:
; APPLICANT: Martijn, Cecile
; APPLICANT: Rondahl, Lena
; TITLE OF INVENTION: THERAPEUTIC PROTEINS
; FILE REFERENCE: 18909-002001
; CURRENT APPLICATION NUMBER: US/11/067,121
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/576,445
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: SE 0400489-1
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0.
; SEQ ID NO 15
; LENGTH: 322
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-067-121-15

```

Query Match	88.7%	Score 848;	DB 7;	Length 322;
Best Local Similarity	99.3%;	Pred. No. 7.2e-78;		
Matches 151;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

QY 21 NCLVOTTEMSACSTKCGMGISRRVINDNASCLEKOSRLCMVRPCADILEENIKKKKKCI 80
Db 171 DCLVOTTEMSACSTKCGMGISRRVINDNASCLEKOSRLCMVRPCADILEENIKKKKKCI 230
QY 81 RTPKISKPIKEBLSGCTSKMTRYARFCGVCTDGRCTPHRTTLLPYEFKCPDGEVNMKNM 140
Db 231 RTPKISKPIKEBLSGCTSKMTRYARFCGVCTDGRCTPHRTTLLPYEFKCPDGEVNMKNM 290


```
Qy 141 MFIKTCACHYNCPGNDIFESLYRKMYGDMA 172
Db 291 MFIKTCACHYNCPGNDIFESLYRKMYGDMA 322

RESULT 6
US-11-094-519A-46
; Sequence 46, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurie
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 46
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-094-519A-46

Query Match 45.2%; Score 433; DB 7; Length 74;
Best Local Similarity 100.0%; Pred. No. 5.3e-37;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 MKTYRAKFCGVCCTDGRCTPHRTTTLVFEKCPDGEVKKMMFIKTCACHYNCPGNDI 158
Db 1 MKTYRAKFCGVCCTDGRCTPHRTTTLVFEKCPDGEVKKMMFIKTCACHYNCPGNDI 60

Qy 159 FESLYRKMYGDMA 172
Db 61 FESLYRKMYGDMA 74

RESULT 7
US-10-131-826A-320
; Sequence 320, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Tuma, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
```

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; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 320
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-320

Query Match 15.5%; Score 148; DB 6; Length 250;
Best Local Similarity 56.8%; Pred. No. 4.3e-08;
Matches 25; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 22 CLVQTTWSACSKTCGMSITRYTNDNASCRLEKQSLCWRPC 65
Db 194 CPEWSTAWGPCSTTCGLGMATRVSNQNFRCLETORRLCLSRPC 237

RESULT 8
US-11-039-398-12
; Sequence 12, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; PRIOR FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1216
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-12

Query Match 10.8%; Score 103.5; DB 7; Length 1216;
Best Local Similarity 22.6%; Pred. No. 0.0061;
Matches 45; Conservative 24; Mismatches 57; Indels 73; Gaps 11;

Qy 15 PMIRANNC-----LVQTTWSACSKTCG-MGISTRYTNDNASCRLEKQSLCWRPC 65
Db 894 PKEIRRCNQHPQSGPVWVTEWAGASRSGKGLGVTR-----GIQCLPLSTGTHVMA 949

Qy 66 EADLEENIKKGGKCIPTPKISKIPKEL---SGCTSMKTYRAKFCG----- 108
```

```
Db      950 KACAGDRPEARPCLRVP---CPAQWRLGAWSCSAT-----CGEGIQORQVVCRTNA 999
Qy      109 -----VCTDRCCTPHRTTLPV---EFKCPDGE-----VMKXNM 140
Db      1000 NSLGHCEGDRPDYQVCSLPACGNGHONSTVRADWELGTPEGQWVPOSGPLHPINKISS 1059
Qy      141 MFIKTCACHYNCPGDNDIF 159
Db      1060 M-----CAAE-PCGTGDRSVF 1073

RESULT 9
US-11-039-398-8
; Sequence 8, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Frididdle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; PRIOR FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1222
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-8

Query Match      10.8%; Score 103.5; DB 7; Length 1222;
Best Local Similarity 22.6%; Pred. No. 0.0062;
Matches 45; Conservative 24; Mismatches 57; Indels 73; Gaps 11;

Qy      15 PTMIRANC-----LVQTTWSACSKTCG-MGISTRTVNDNASCRLEKQSLCMVRPC 65
Db      894 PKPIRRRCNQHPCSQPVWVTEWGCASRSCGLGVQTR-----GIQCLPLSLNGTHKWPFA 949
Qy      66 EADLEENIKKKGKCTIRPKISKPIKFEI---SGCTSMKTYRAKFCG-----108
Db      950 KACAGDRPEARPCLRVP---CPAQWRLGAWSCSAT-----CGEGIQORQVVCRTNA 999
Qy      109 -----VCTDRCCTPHRTTLPV---EFKCPDGE-----VMKXNM 140
Db      1000 NSLGHCEGDRPDYQVCSLPACGNGHONSTVRADWELGTPEGQWVPOSGPLHPINKISS 1059
Qy      141 MFIKTCACHYNCPGDNDIF 159
Db      1060 M-----CAAE-PCGTGDRSVF 1073

RESULT 10
US-11-039-398-16
; Sequence 16, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Frididdle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomichy, Boris
; APPLICANT: Hu, Yi
```

```
; TITLE OF INVENTION: Novel Human Proteases and
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; PRIOR FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1235
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-16

Query Match      10.8%; Score 103.5; DB 7; Length 1235;
Best Local Similarity 22.6%; Pred. No. 0.0062;
Matches 45; Conservative 24; Mismatches 57; Indels 73; Gaps 11;

Qy      15 PTMIRANC-----LVQTTWSACSKTCG-MGISTRTVNDNASCRLEKQSLCMVRPC 65
Db      894 PKPIRRRCNQHPCSQPVWVTEWGCASRSCGLGVQTR-----GIQCLPLSLNGTHKWPFA 949
Qy      66 EADLEENIKKKGKCTIRPKISKPIKFEI---SGCTSMKTYRAKFCG-----108
Db      950 KACAGDRPEARPCLRVP---CPAQWRLGAWSCSAT-----CGEGIQORQVVCRTNA 999
Qy      109 -----VCTDRCCTPHRTTLPV---EFKCPDGE-----VMKXNM 140
Db      1000 NSLGHCEGDRPDYQVCSLPACGNGHONSTVRADWELGTPEGQWVPOSGPLHPINKISS 1059
Qy      141 MFIKTCACHYNCPGDNDIF 159
Db      1060 M-----CAAE-PCGTGDRSVF 1073

RESULT 11
US-11-039-398-20
; Sequence 20, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Frididdle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; PRIOR FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 1252
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-20

Query Match      10.8%; Score 103.5; DB 7; Length 1252;
Best Local Similarity 22.6%; Pred. No. 0.0063;
Matches 45; Conservative 24; Mismatches 57; Indels 73; Gaps 11;
```

```
Oy 15 PTMIRANC-----LVQTEWSACSKTCG-MGISTRVTNDNASCRLEKOSRLCMVRPC 65
Db 894 PKPIRRRCQHPCSPQVWYTEMGACSRSCGLGVOTR-----GIQCLPLNSGTHKVMRA 949
Oy 66 EADLEENIKKKKCIKRTPKISKIPKEL---SGCTSMKTYRAKFCG-----108
Db 950 KACAGDRPEARPCLRVP---CPAQWRLGAMWSQCSAT-----CSEGIGQORQVCRINA 999
Oy 109 -----VCTDGRCTPHRTTLPV---EFKCPDGE-----VMKQNM 140
Db 1000 NSLGHCEGDRPDTVQVCSLPACGNGHNSITVADVWELGTPEQWVPOSGPLHPINKISS 1059
Oy 141 MFIKTCACHYNCPGDNDIF 159
Db 1060 M-----CAAE-PCTGDRSVF 1073
```

```
RESULT 12
US-11-039-398-14
; Sequence 14, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/11/039,398
; PRIOR FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1213
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-14
```

```
Query Match 10.7%; Score 102; DB 7; Length 1213;
Best Local Similarity 22.0%; Pred. No. 0.0087;
Matches 42; Conservative 27; Mismatches 62; Indels 60; Gaps 9;

Oy 15 PTMIRANC-----LVQTEWSACSKTCG-MGISTRVTNDNASCRLEKOSRLCMVRPC 65
Db 894 PKPIRRRCQHPCSPQVWYTEMGACSRSCGLGVOTR-----GIQCLPLNSGTHKVMRA 949
Oy 66 EADLEENIKKKKCIKRTPKISKIPKEL---SGCTSMKTYRAKFCG-----108
Db 950 KACAGDRPEARPCLRVP---CPAQWRLGAMWSQCSAT-----CSEGIGQORQVCRINA 999
Oy 109 -----VCTDGRCTPHRTTLPV---EFKCPDGEVMKQNM-MMFITCACC 148
Db 1000 NSLGHCEGDRPDTVQVCSLPACGNGHNSITVADVWELGTPEQWVPOSGPLHPINKISS 1059
Oy 149 HYNCPGDNDIF 159
Db 1060 TEPCTGDRSVF 1070
```

```
RESULT 13
US-11-039-398-10
; Sequence 10, Application US/11039398.
; Publication No. US20050267297A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/11/039,398
; PRIOR FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1219
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-10
```

```
Query Match 10.7%; Score 102; DB 7; Length 1219;
Best Local Similarity 22.0%; Pred. No. 0.0087;
Matches 42; Conservative 27; Mismatches 62; Indels 60; Gaps 9;

Oy 15 PTMIRANC-----LVQTEWSACSKTCG-MGISTRVTNDNASCRLEKOSRLCMVRPC 65
Db 894 PKPIRRRCQHPCSPQVWYTEMGACSRSCGLGVOTR-----GIQCLPLNSGTHKVMRA 949
Oy 66 EADLEENIKKKKCIKRTPKISKIPKEL---SGCTSMKTYRAKFCG-----108
Db 950 KACAGDRPEARPCLRVP---CPAQWRLGAMWSQCSAT-----CSEGIGQORQVCRINA 999
Oy 109 -----VCTDGRCTPHRTTLPV---EFKCPDGEVMKQNM-MMFITCACC 148
Db 1000 NSLGHCEGDRPDTVQVCSLPACGNGHNSITVADVWELGTPEQWVPOSGPLHPINKISS 1059
Oy 149 HYNCPGDNDIF 159
Db 1060 TEPCTGDRSVF 1070
```

```
RESULT 14
US-11-039-398-18
; Sequence 18, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/11/039,398
; PRIOR FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1232
```

TYPE: PRT
ORGANISM: homo sapiens
US-11-039-398-18

Query Match 10.7%; Score 102; DB 7; Length 1232;
Best Local Similarity 22.0%; Pred. No. 0.0088;
Matches 42; Conservative 27; Mismatches 62; Indels 60; Gaps 9;

QY 15 PTMIRANC-----LVQTEMSASCKTCG-MGISTRTVNDNASCRLEKOSRLCMWRPC 65
DB 894 PKPIRRRCNQHPCSPVWVTEMGACSRSCGKLGVQTR---GIQCLPLSNGTHKWMPA 949
QY 66 EADLEENIKKGKCIKRTPKISKPIKFEY---SGCTSMKTYRAKFCG----- 108
DB 950 KACAGDRPEARPCLRVP---CPAOWRLGAMWQCSAT-----CGEGIOQROVVCRTNA 999
QY 109 -----VCTDGRCTPHRTTTLPLV---EFKCPDGEVWKKN--MMFIKTCAC 148
DB 1000 NSLGHCEGDRPDYQVCSLPAACGNGHNSYTRADVWELGTPEQWVPQSGPLHPINKISS 1059
QY 149 HYNCPGNDIF 159
DB 1060 TEPCGTGDRSVF 1070

RESULT 15
US-11-039-398-22
Sequence 22, Application US/11039398
Publication No. US20050267297A1
GENERAL INFORMATION:
APPLICANT: Fiddler, Carl Johan
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
APPLICANT: Nepomichy, Boris
APPLICANT: Hu, Yi
TITLE OF INVENTION: Novel Human Proteases and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0221-USA
CURRENT APPLICATION NUMBER: US/11/039,398
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US/09/938,330
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: US 60/227,104
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 60/233,796
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 1249
TYPE: PRT
ORGANISM: homo sapiens
US-11-039-398-22

Query Match 10.7%; Score 102; DB 7; Length 1249;
Best Local Similarity 22.0%; Pred. No. 0.0089;
Matches 42; Conservative 27; Mismatches 62; Indels 60; Gaps 9;

QY 15 PTMIRANC-----LVQTEMSASCKTCG-MGISTRTVNDNASCRLEKOSRLCMWRPC 65
DB 894 PKPIRRRCNQHPCSPVWVTEMGACSRSCGKLGVQTR---GIQCLPLSNGTHKWMPA 949
QY 66 EADLEENIKKGKCIKRTPKISKPIKFEY---SGCTSMKTYRAKFCG----- 108
DB 950 KACAGDRPEARPCLRVP---CPAOWRLGAMWQCSAT-----CGEGIOQROVVCRTNA 999
QY 109 -----VCTDGRCTPHRTTTLPLV---EFKCPDGEVWKKN--MMFIKTCAC 148
DB 1000 NSLGHCEGDRPDYQVCSLPAACGNGHNSYTRADVWELGTPEQWVPQSGPLHPINKISS 1059
QY 149 HYNCPGNDIF 159

DB 1060 TEPCGTGDRSVF 1070
Search completed: January 9, 2006, 11:31:22
Job time : 28 secs